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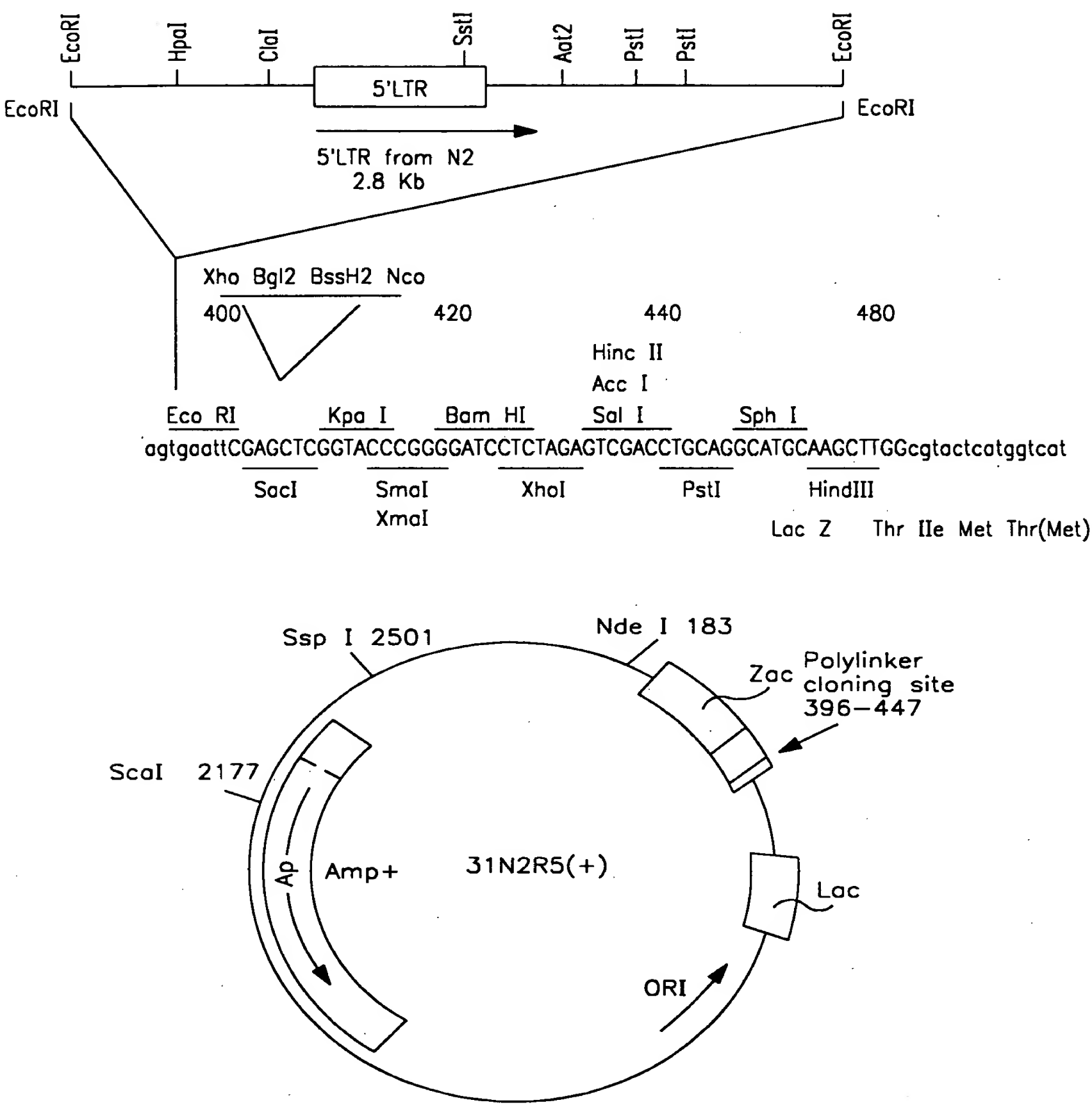


FIG. 1

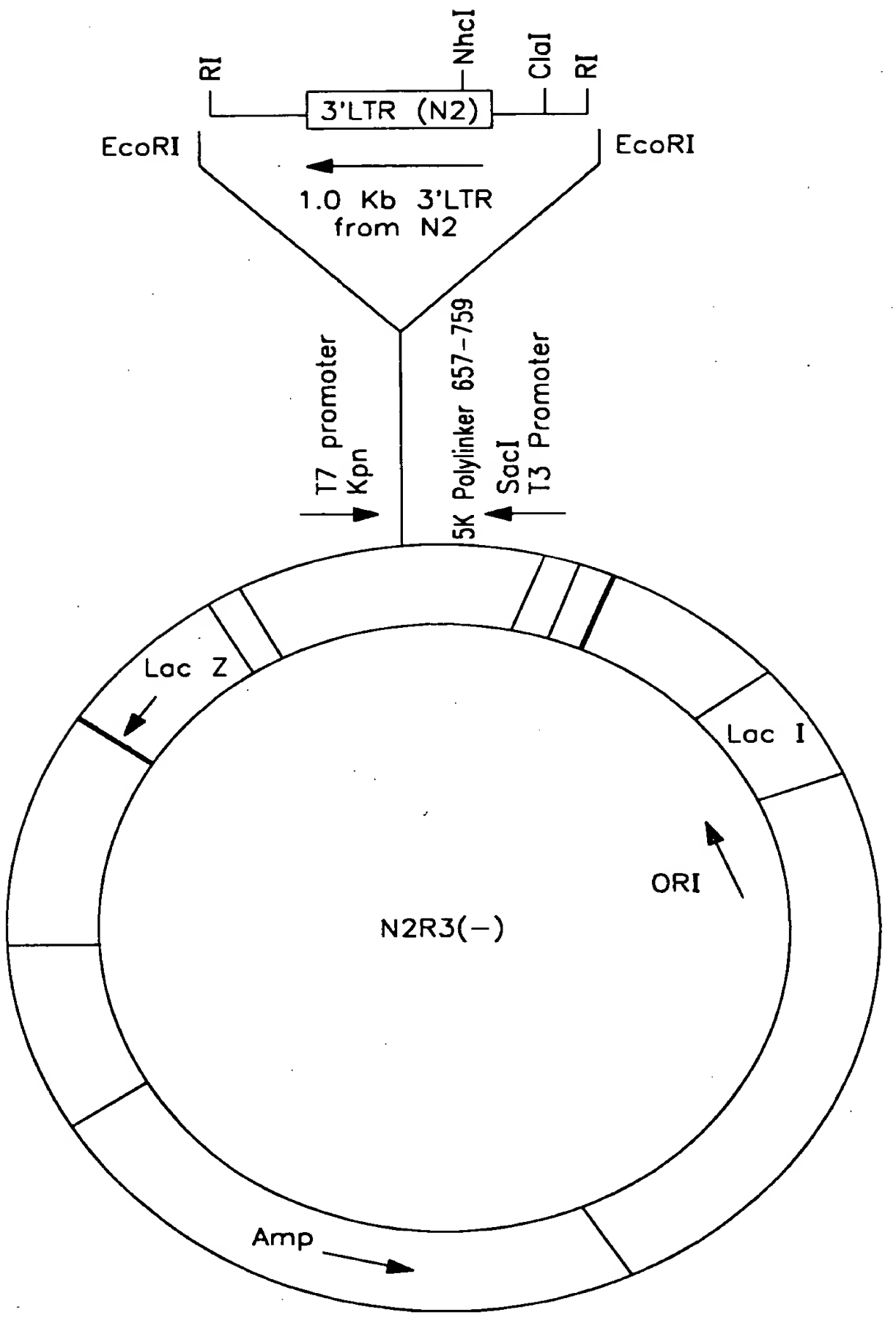


FIG. 2

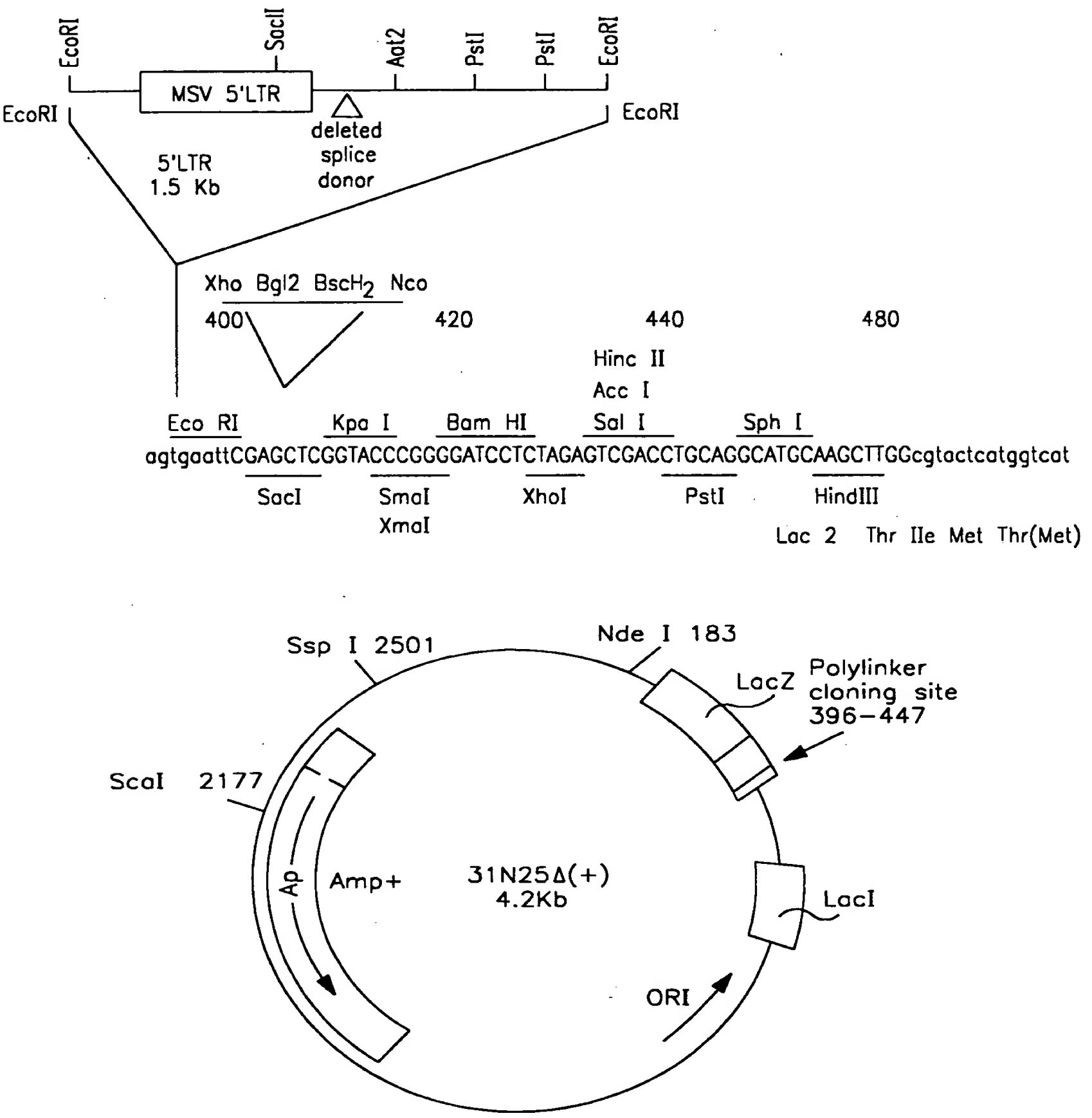


FIG. 3

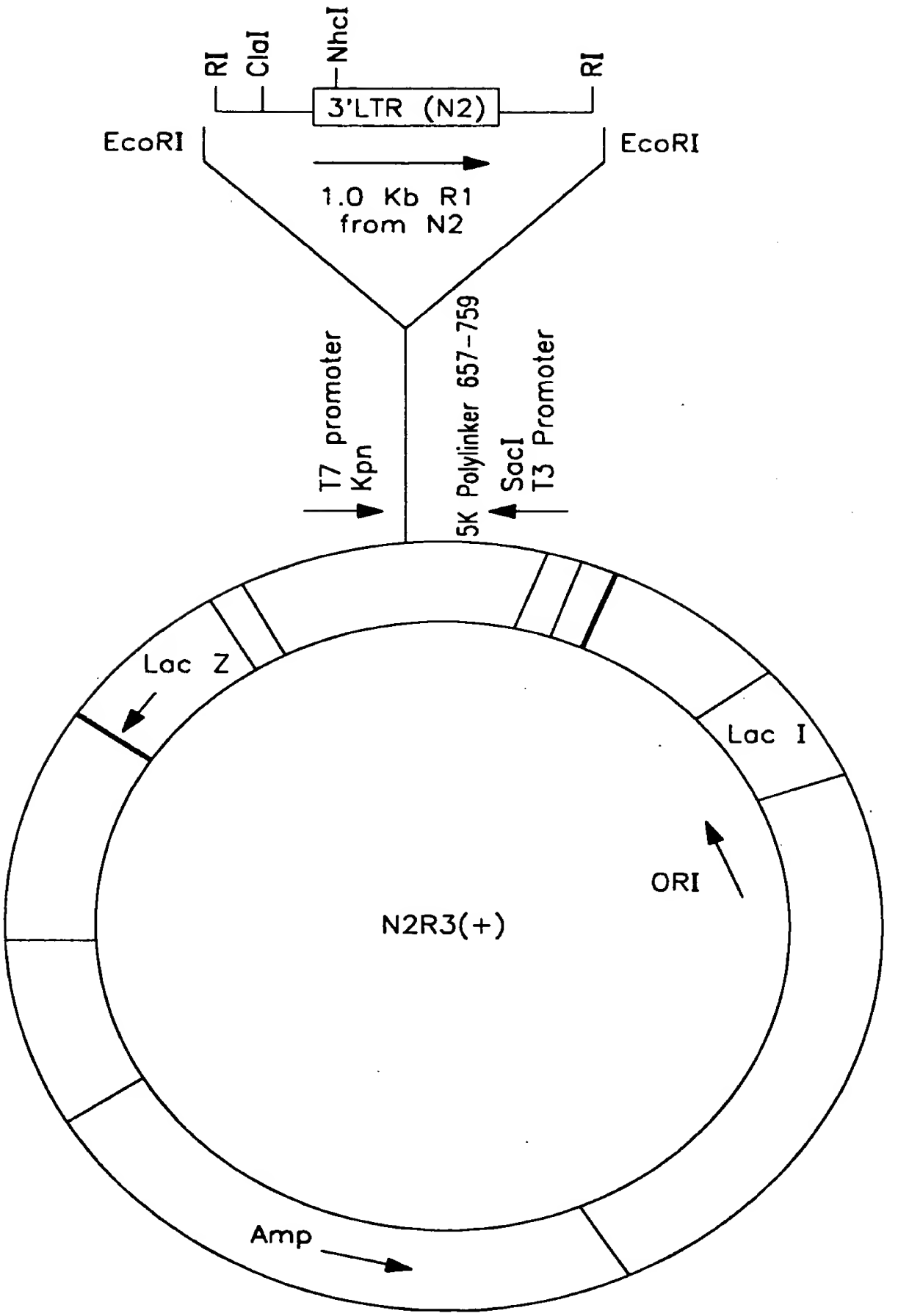


FIG. 4

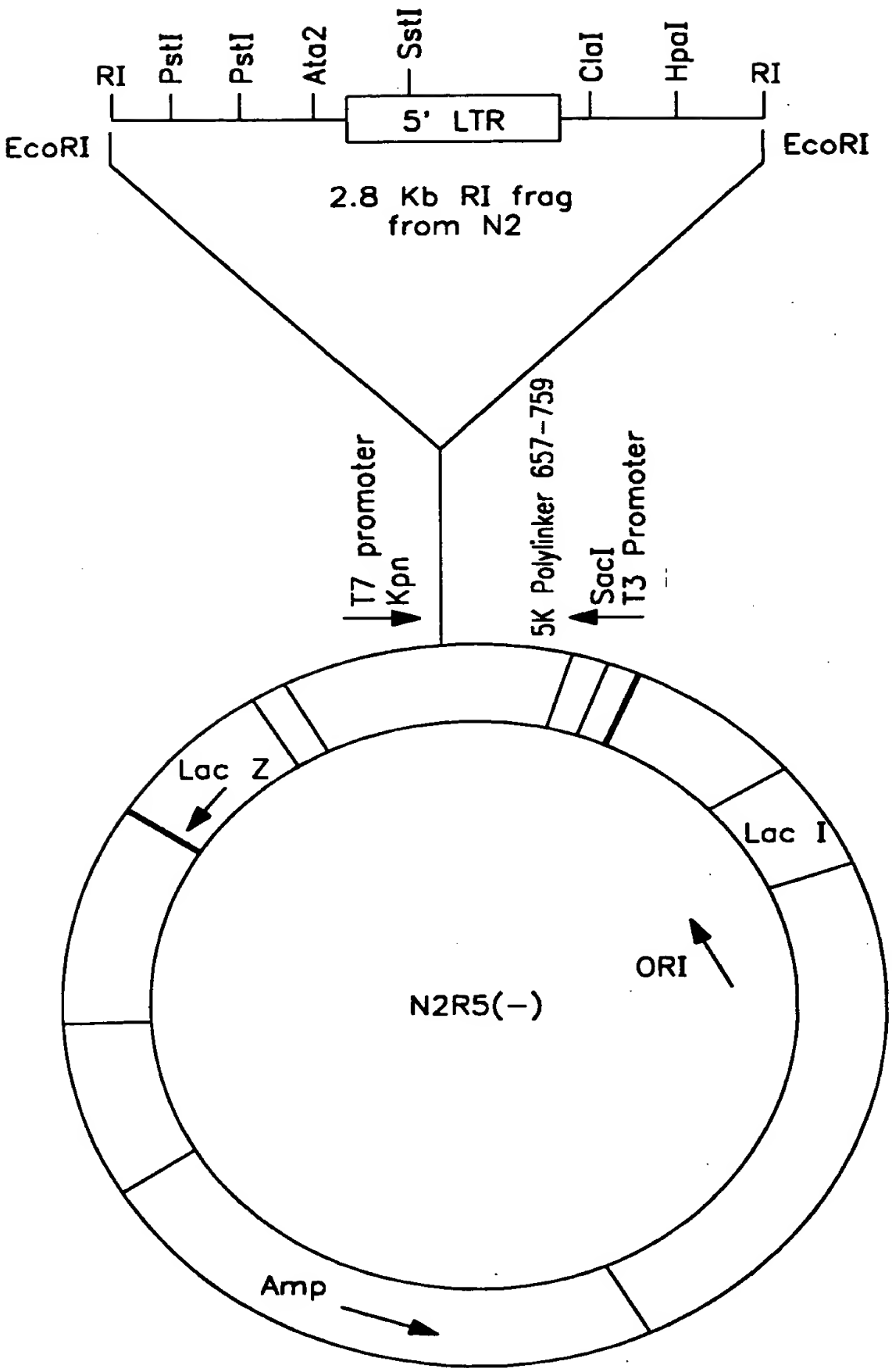


FIG. 5

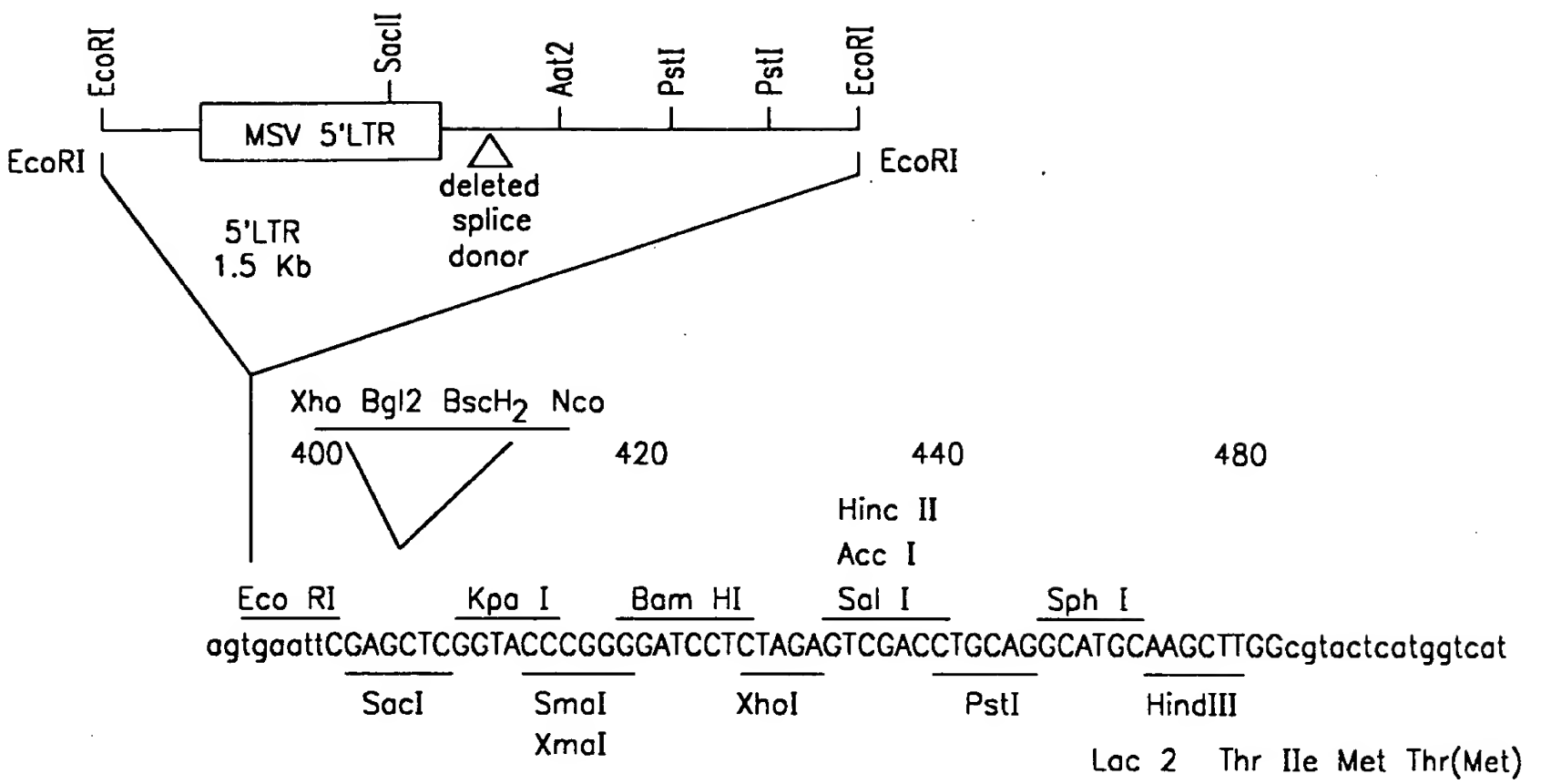
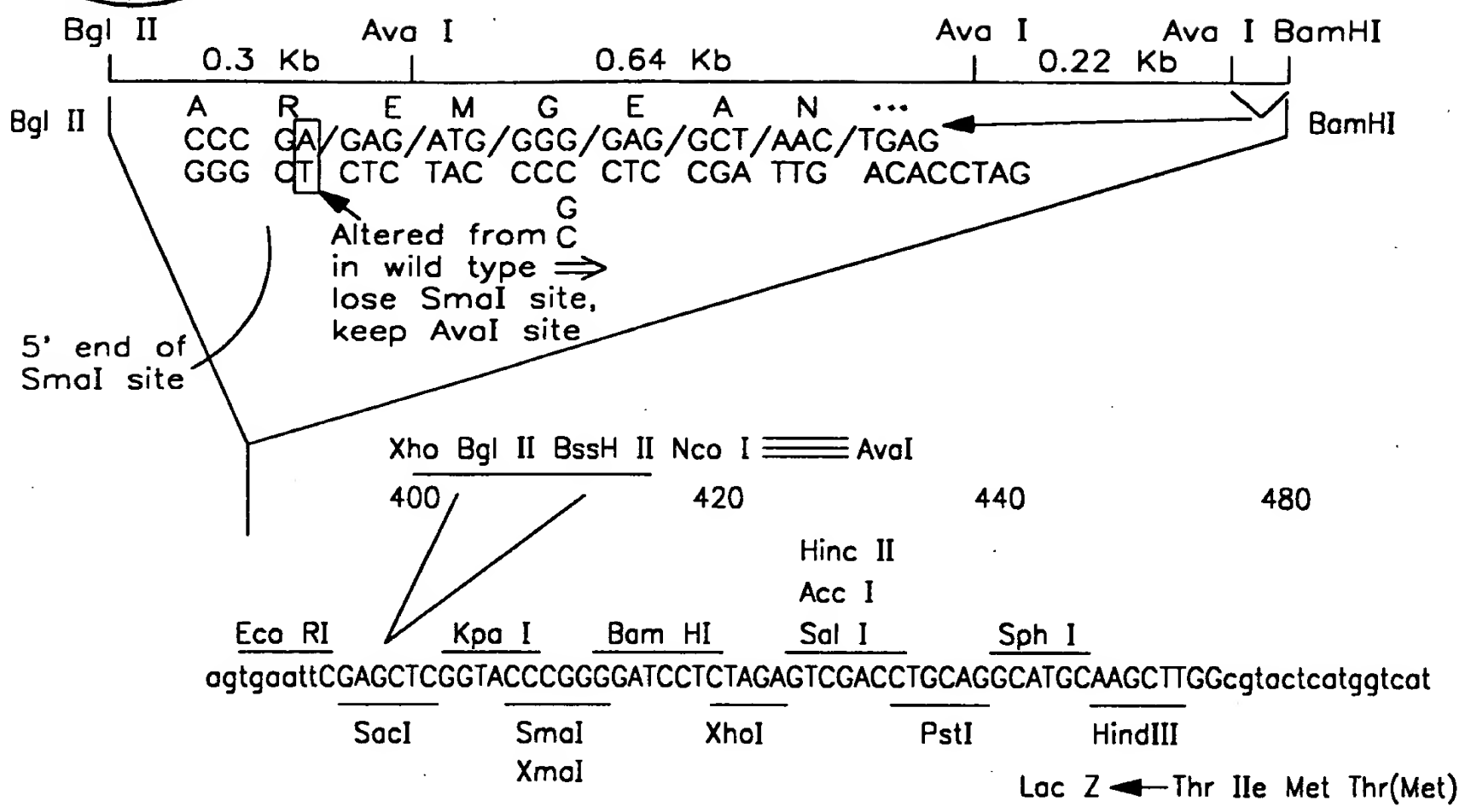


FIG. 6



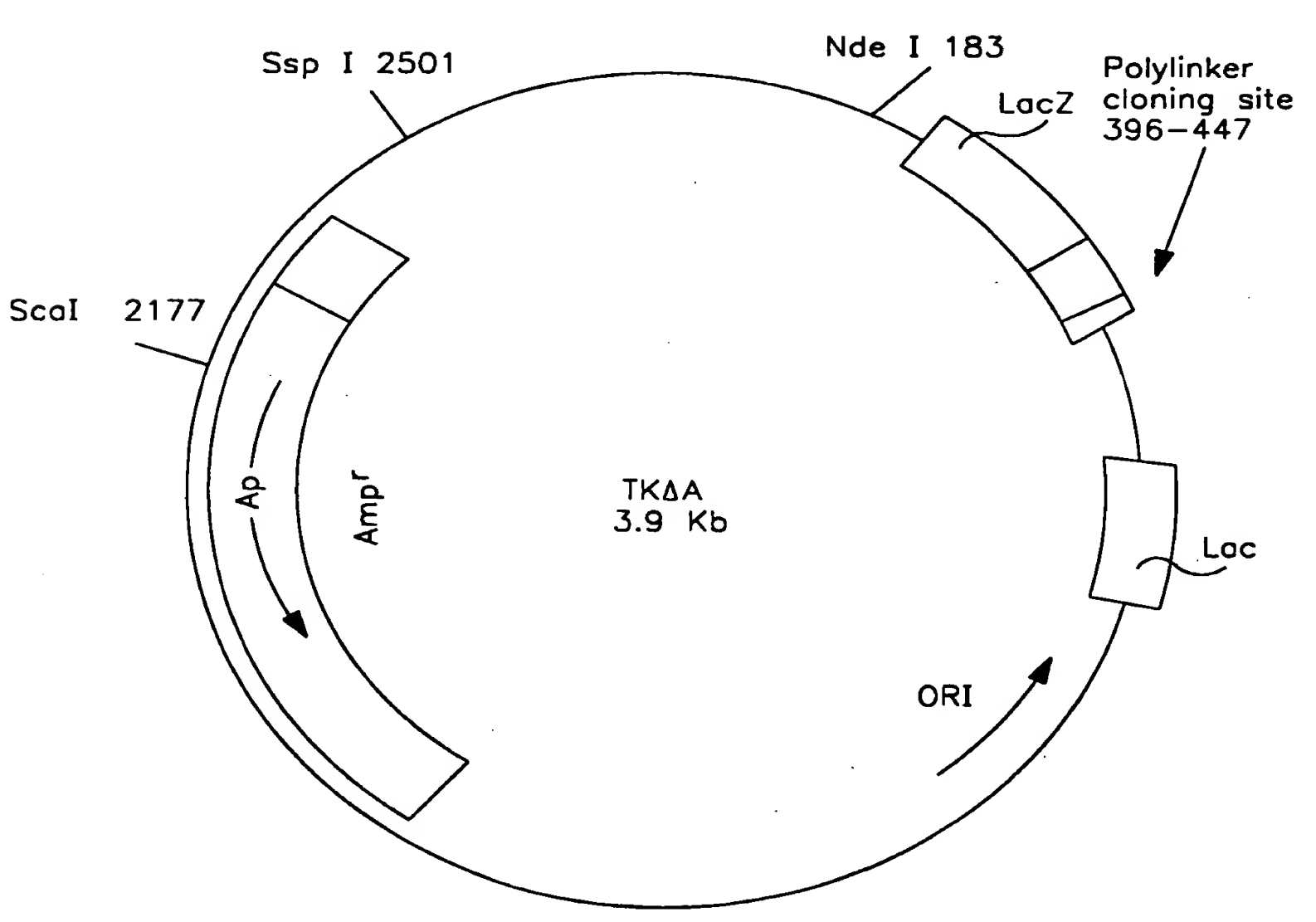


FIG. 7

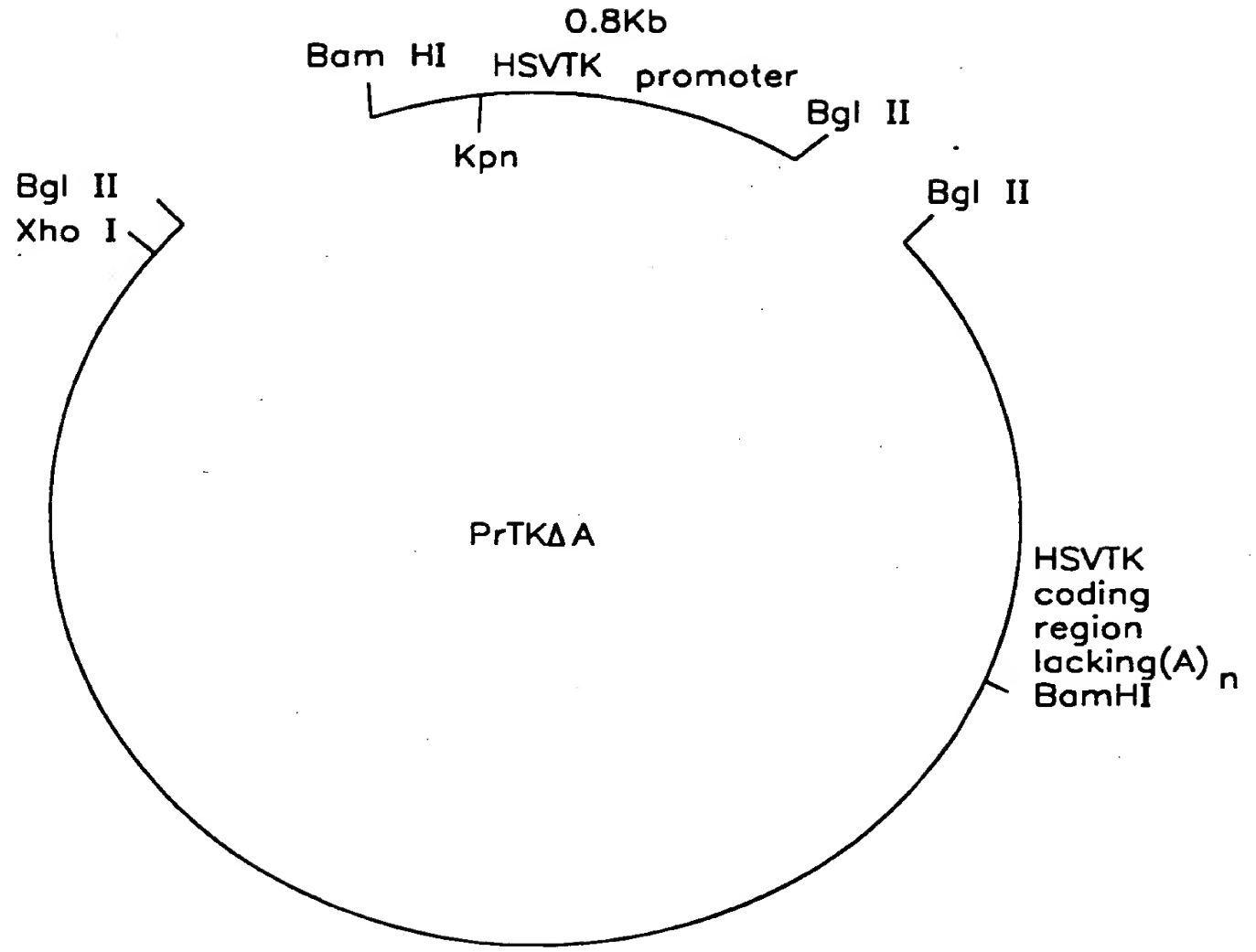


FIG. 8

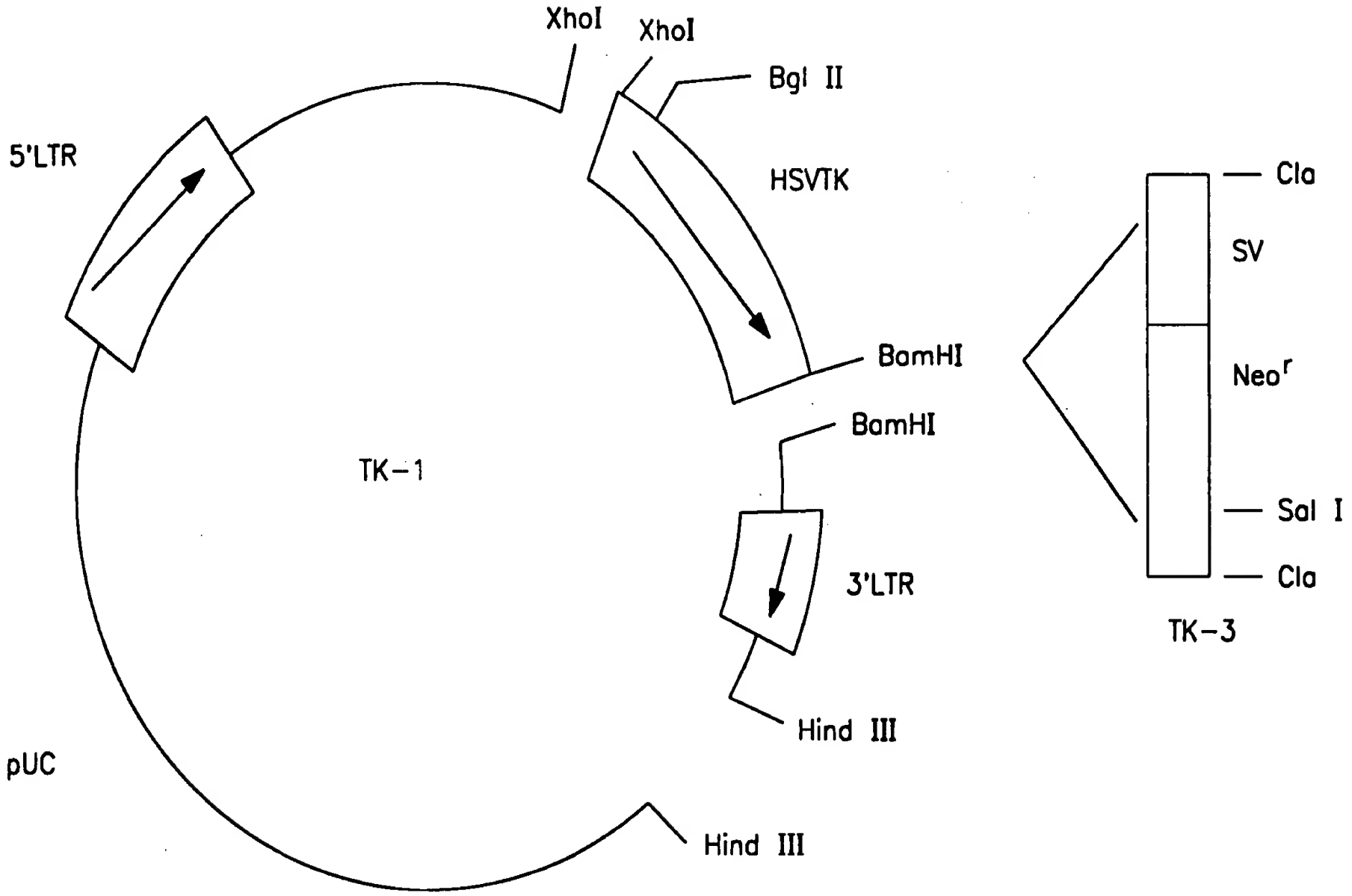


FIG. 9

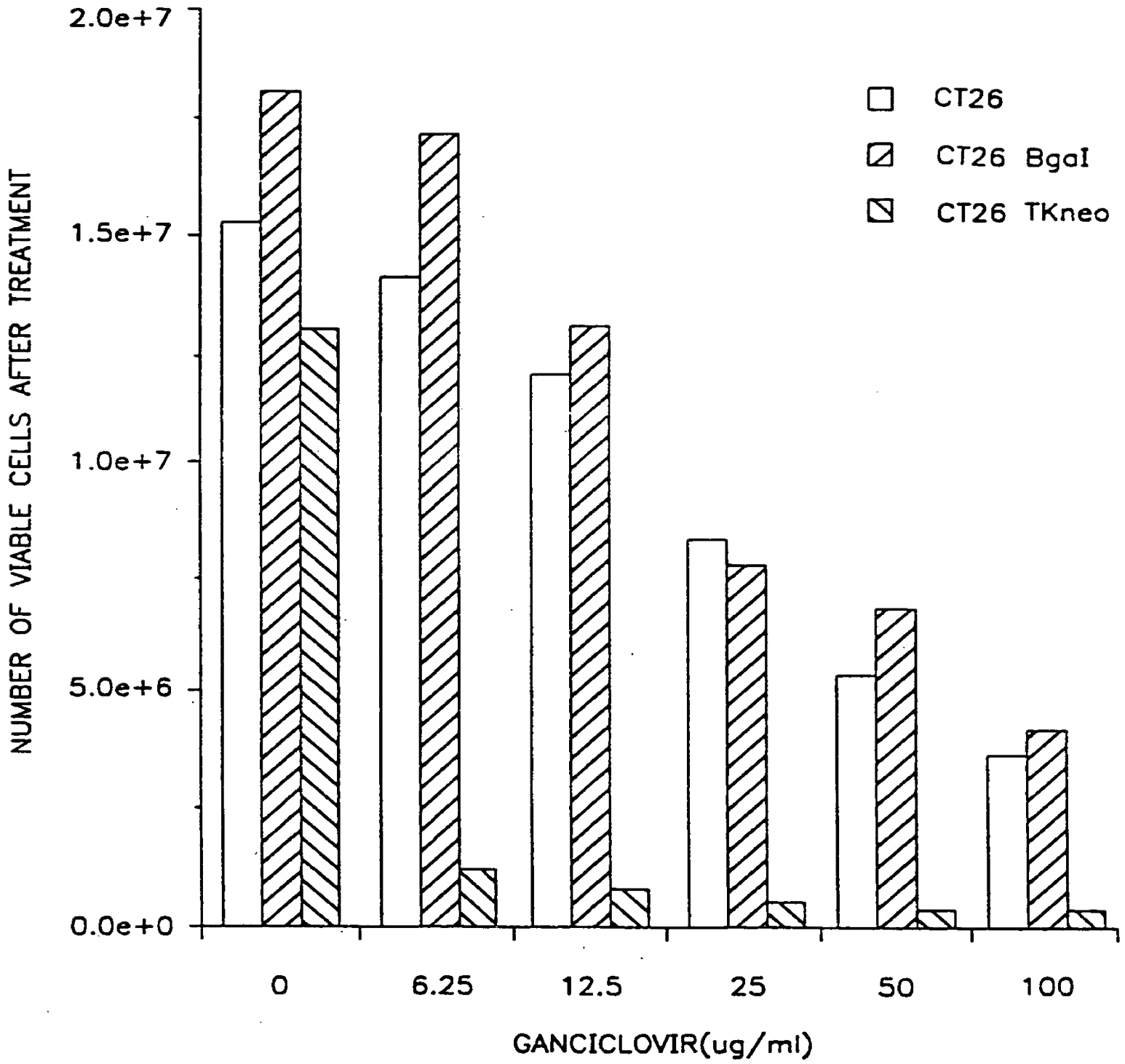


FIG. 10

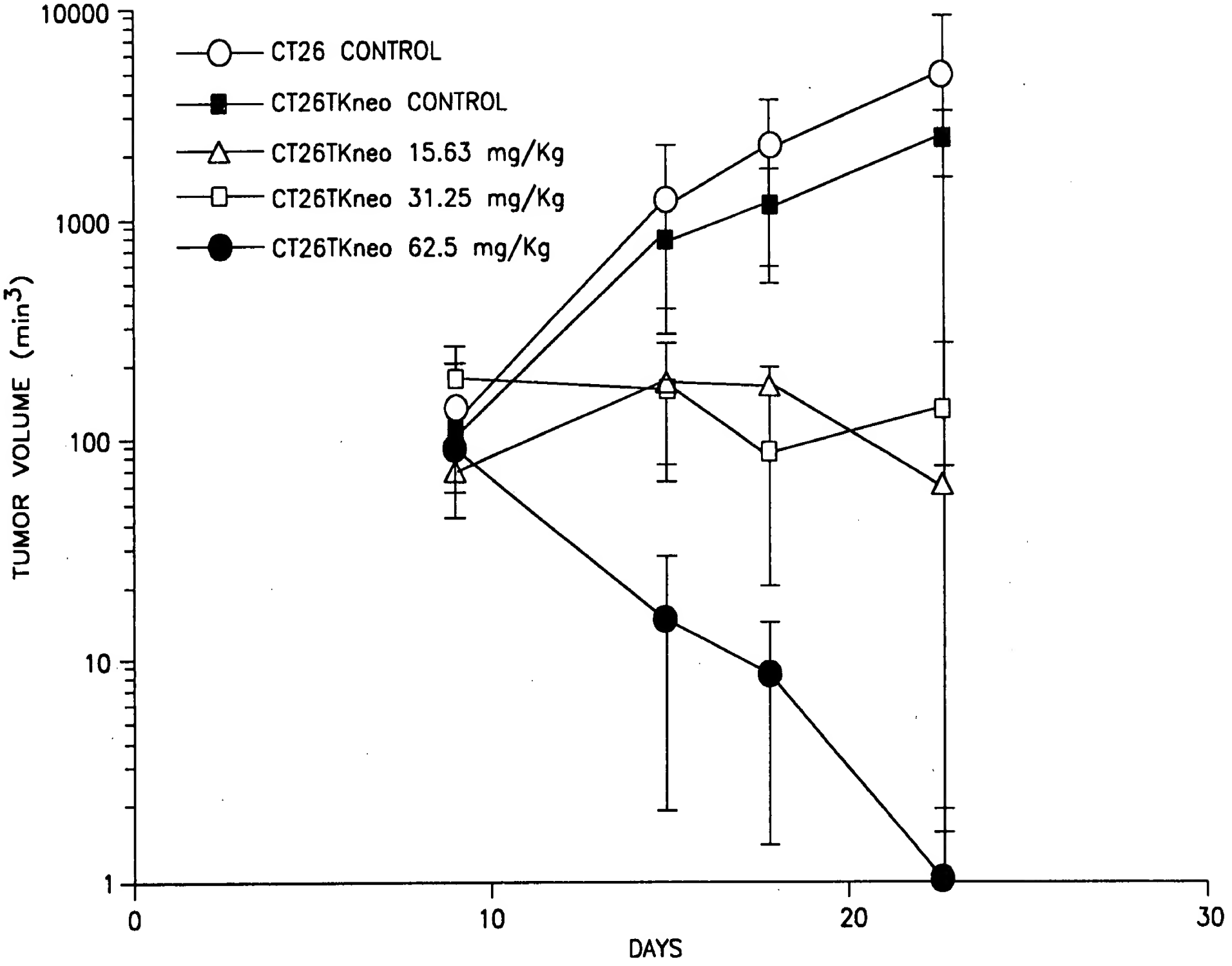


FIG. 11

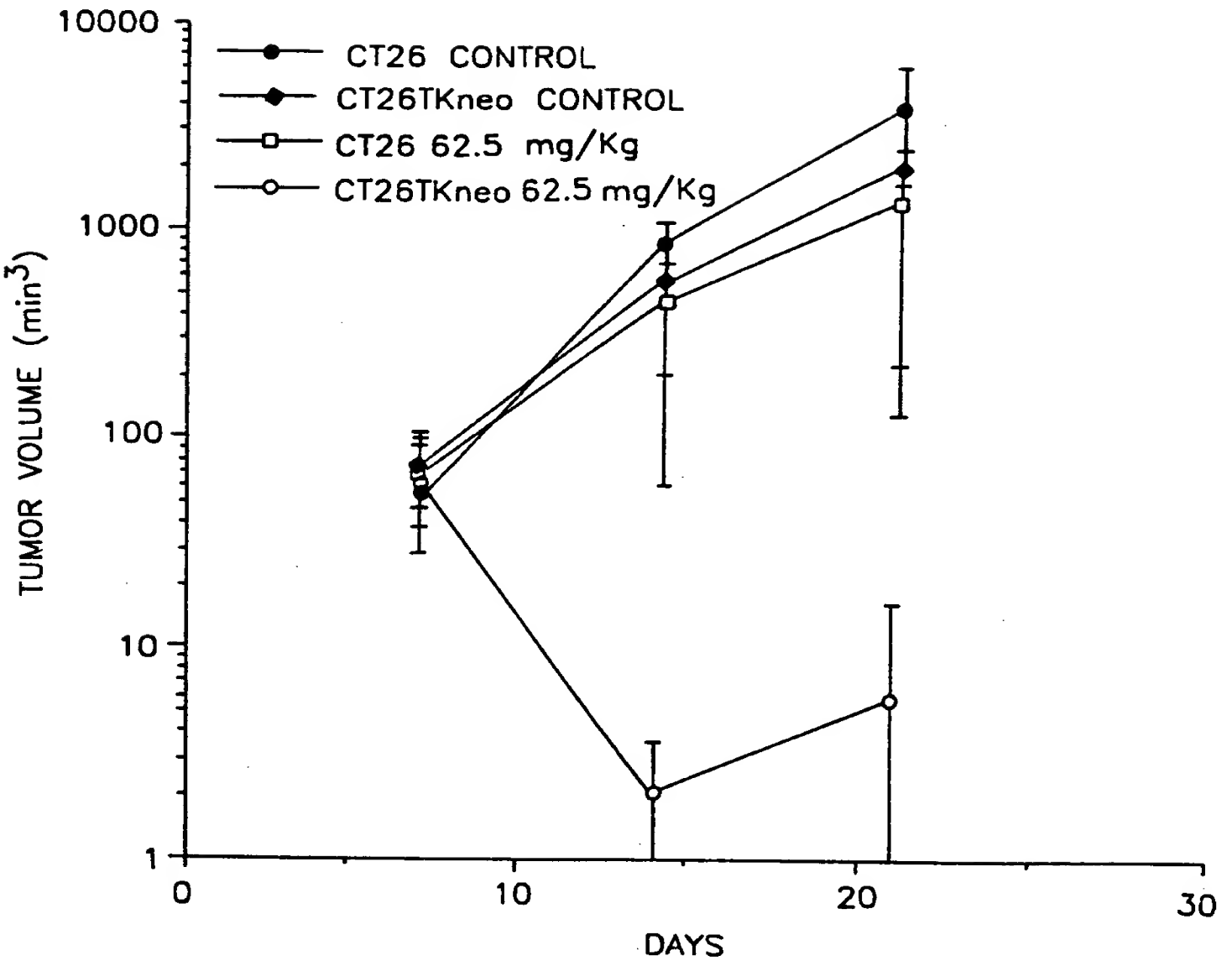
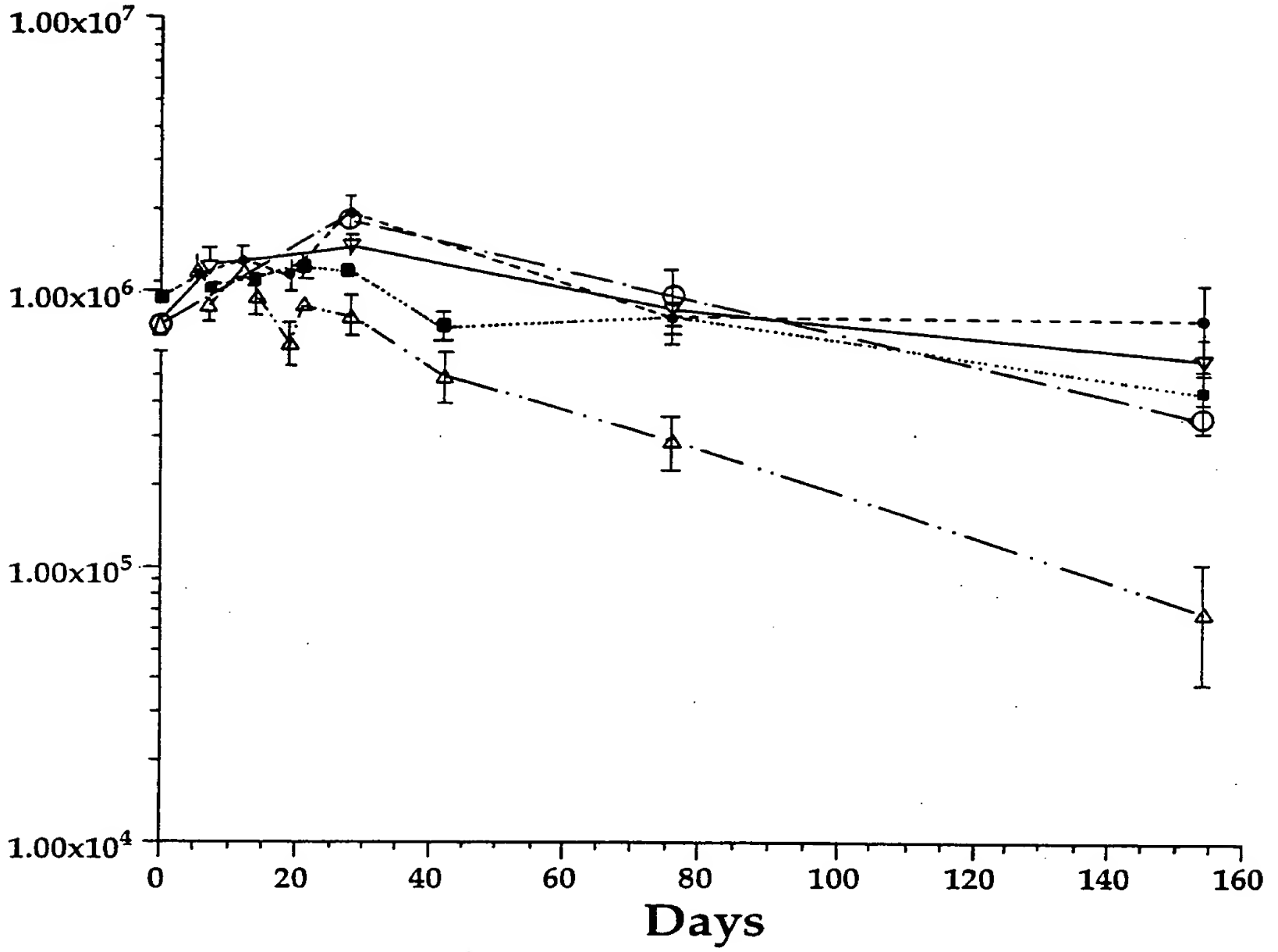


FIG. 12



Formulation:

25mM Tris pH 7.2
60mM NaCl
1 mg/ml Arginine
5 mg/ml HSA
50 mg/ml Lactose

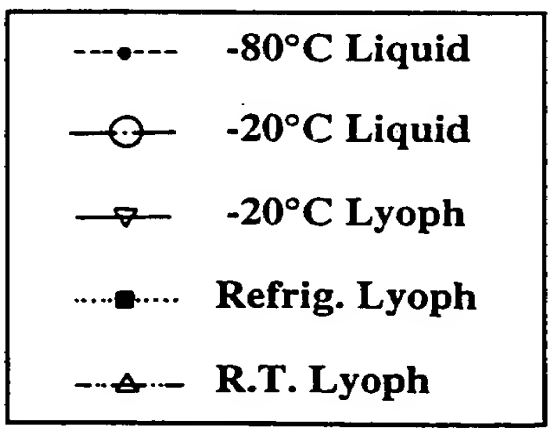
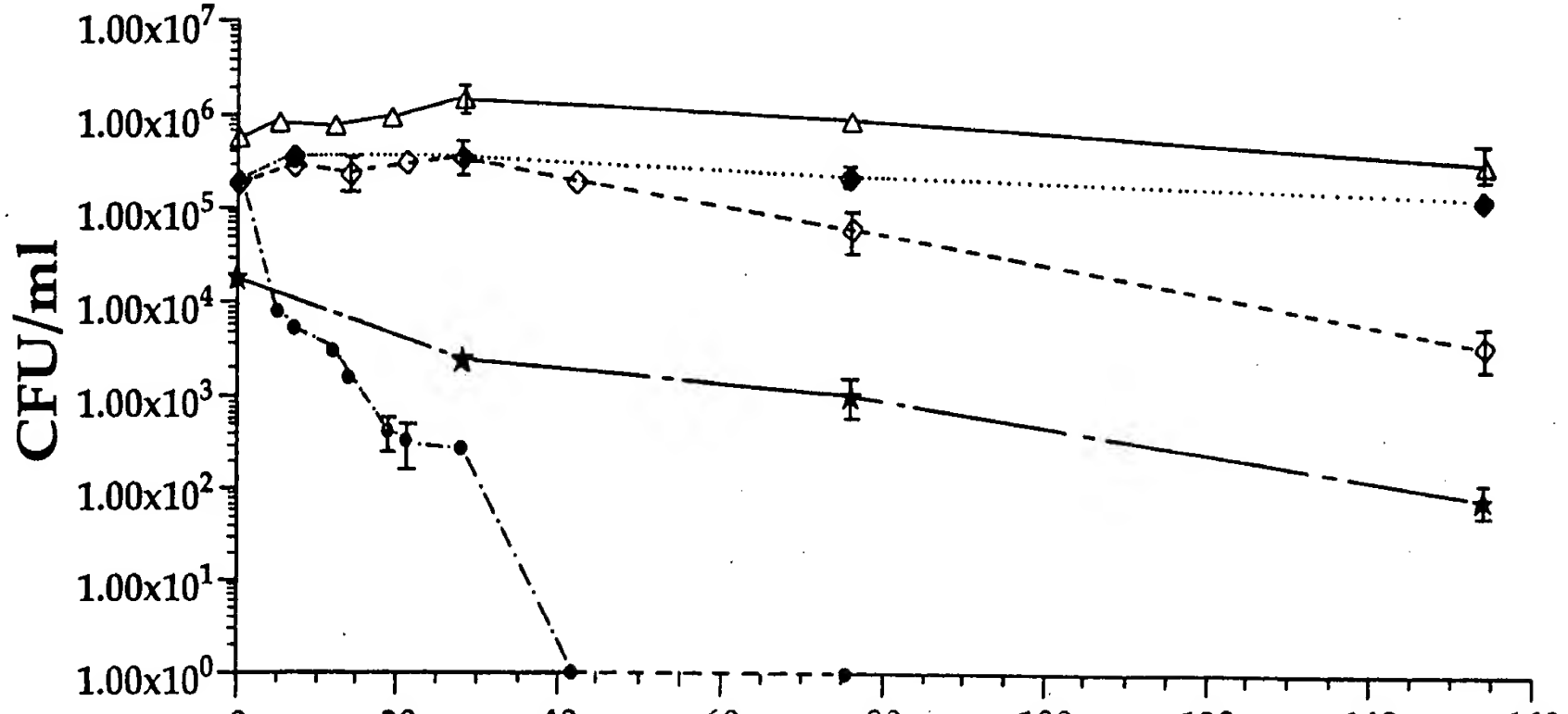


FIG. 13

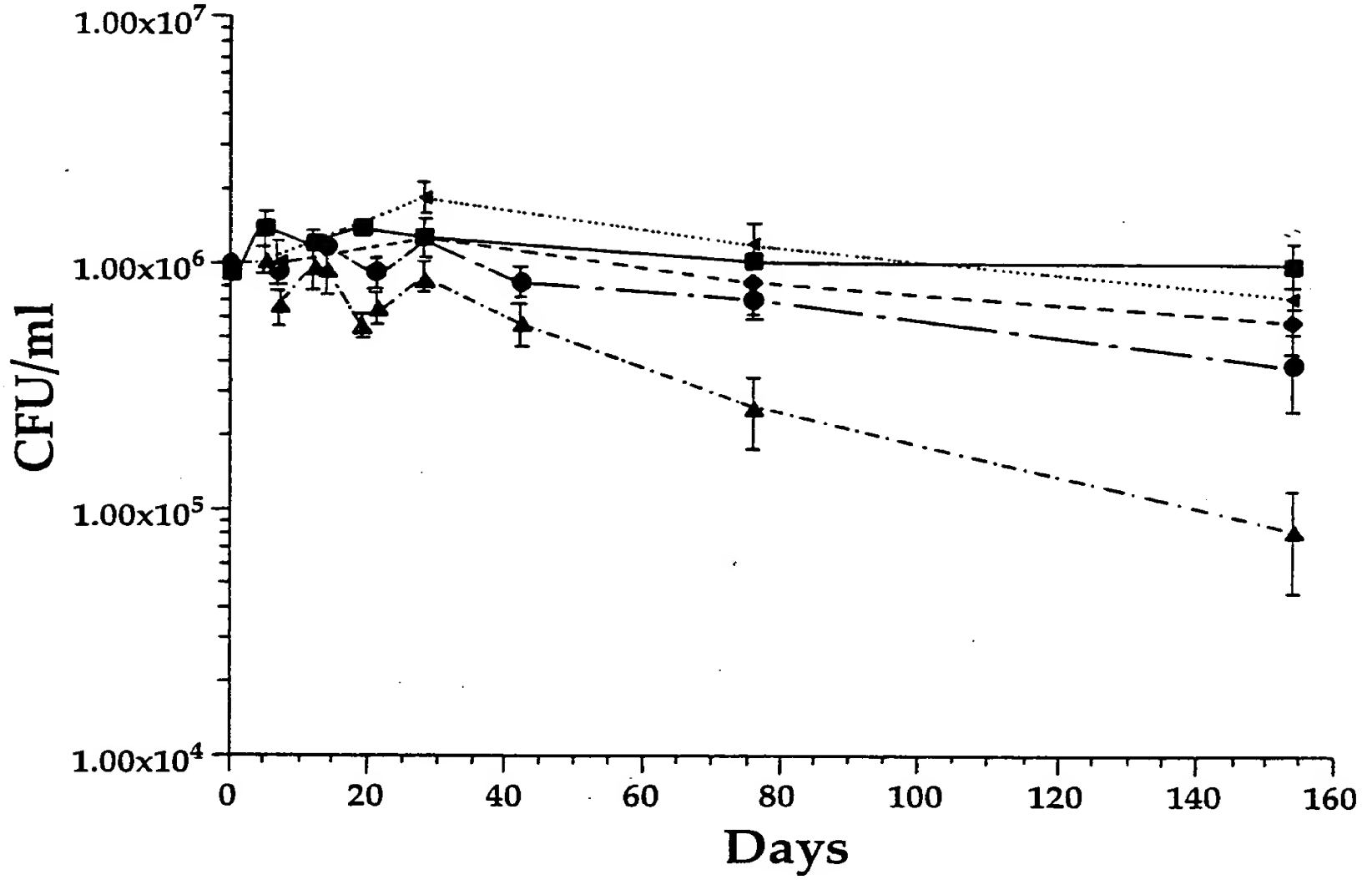


Formulation:

- 25mM Tris pH 7.2
- 25mM NaCl
- 1 mg/ml Arginine
- 5 mg/ml HSA
- 40 mg/ml Mannitol

-80°C Liquid
-20°C Liquid
-20°C Lyoph
Refrig. Lyoph
R.T. Lyoph

FIG. 14



Formulation:

25mM Tris pH 7.2
60mM NaCl
1mg/ml Arginine
5mg/ml HSA
50mg/ml Trehalose

-80°C Liquid
-20°C Liquid
-20°C Lyoph
Refrig. Lyoph
R.T. Lyoph

FIG. 15

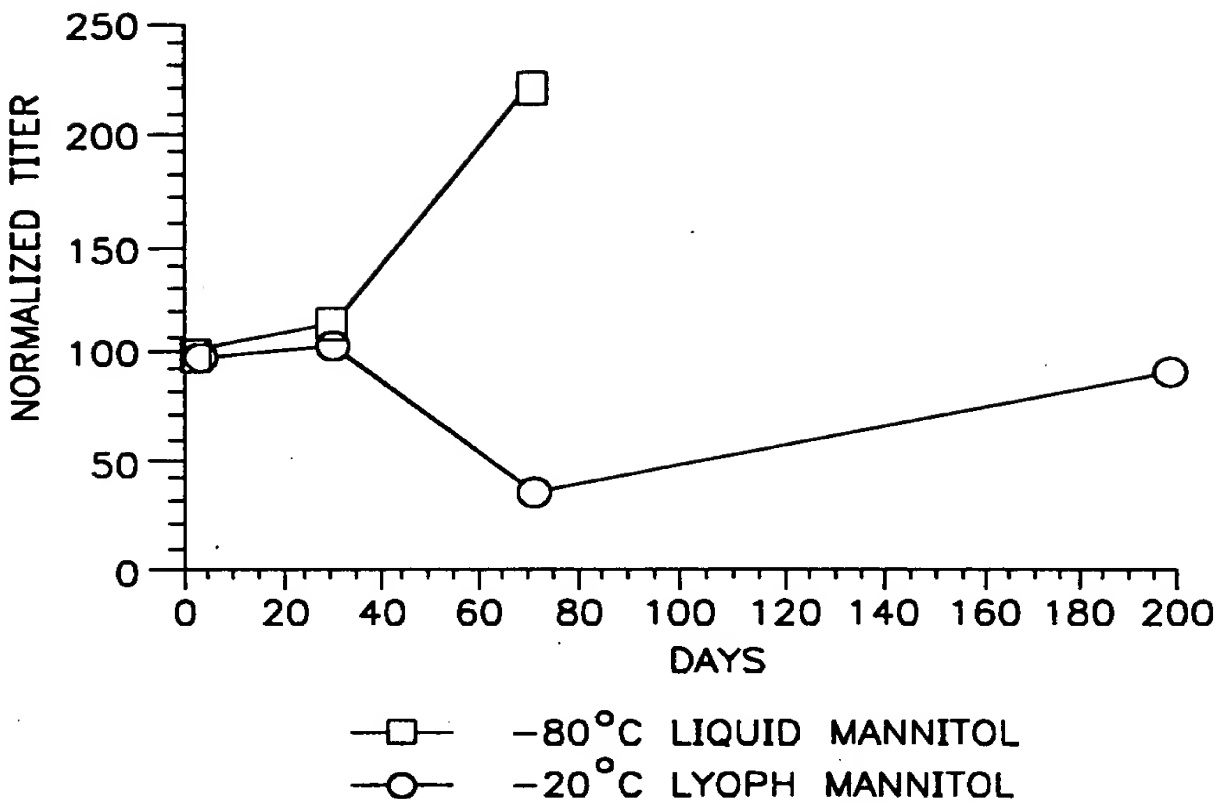


FIG. 16A

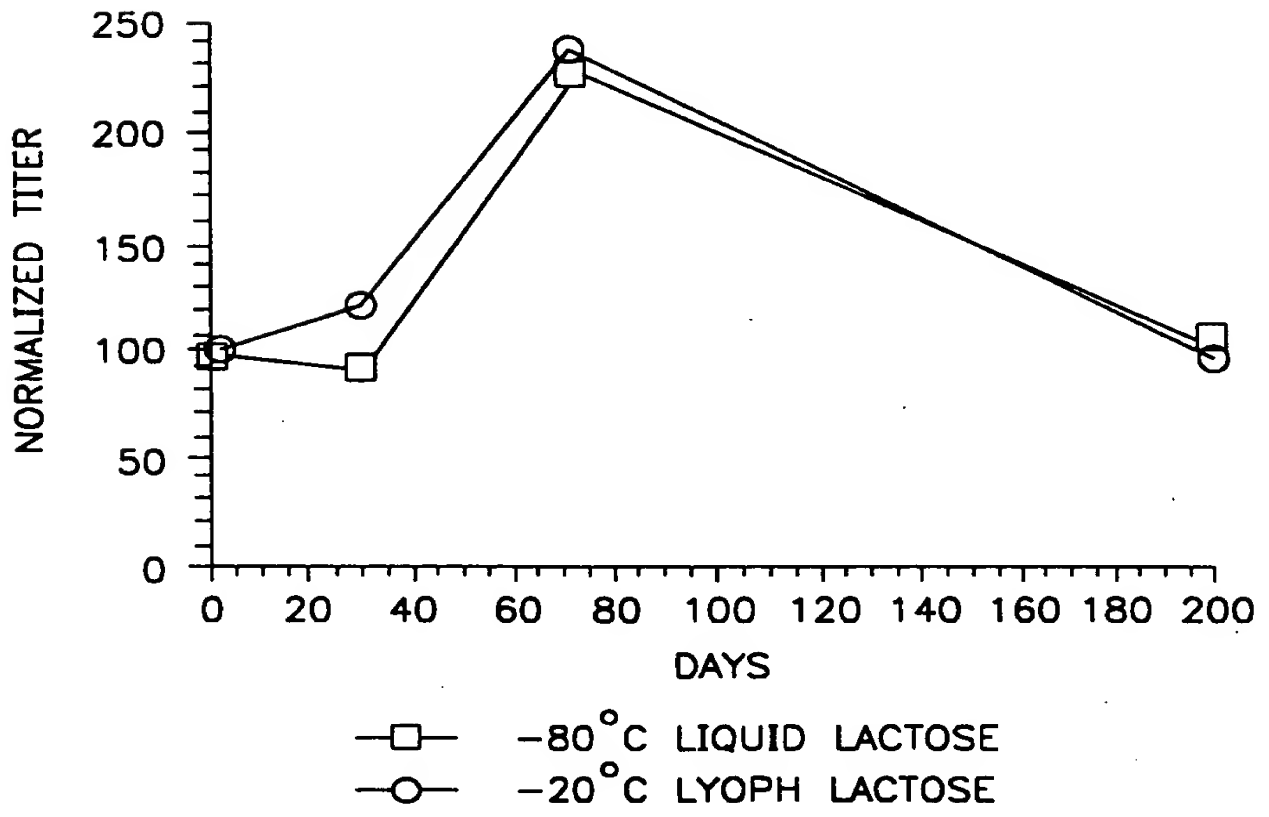


FIG 16B

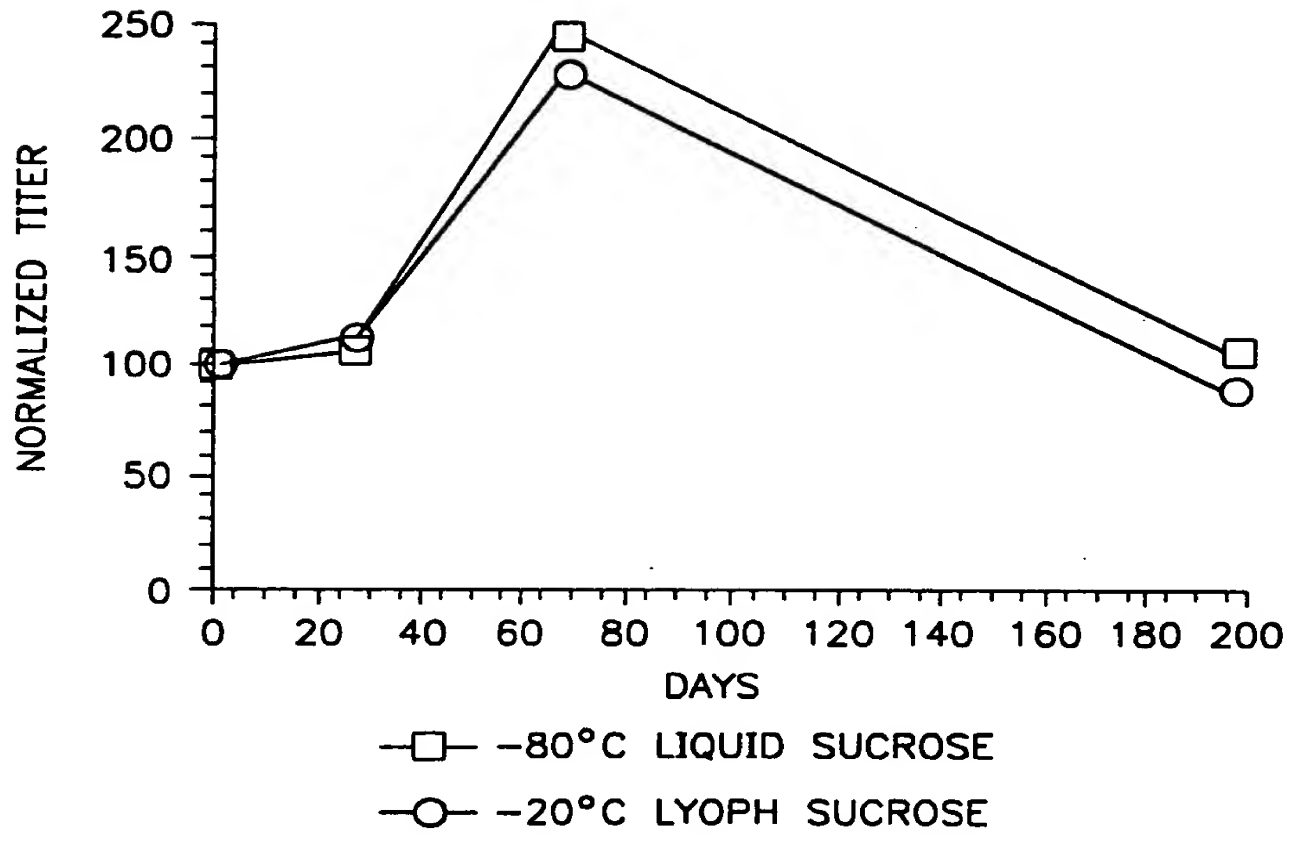


FIG. 16C

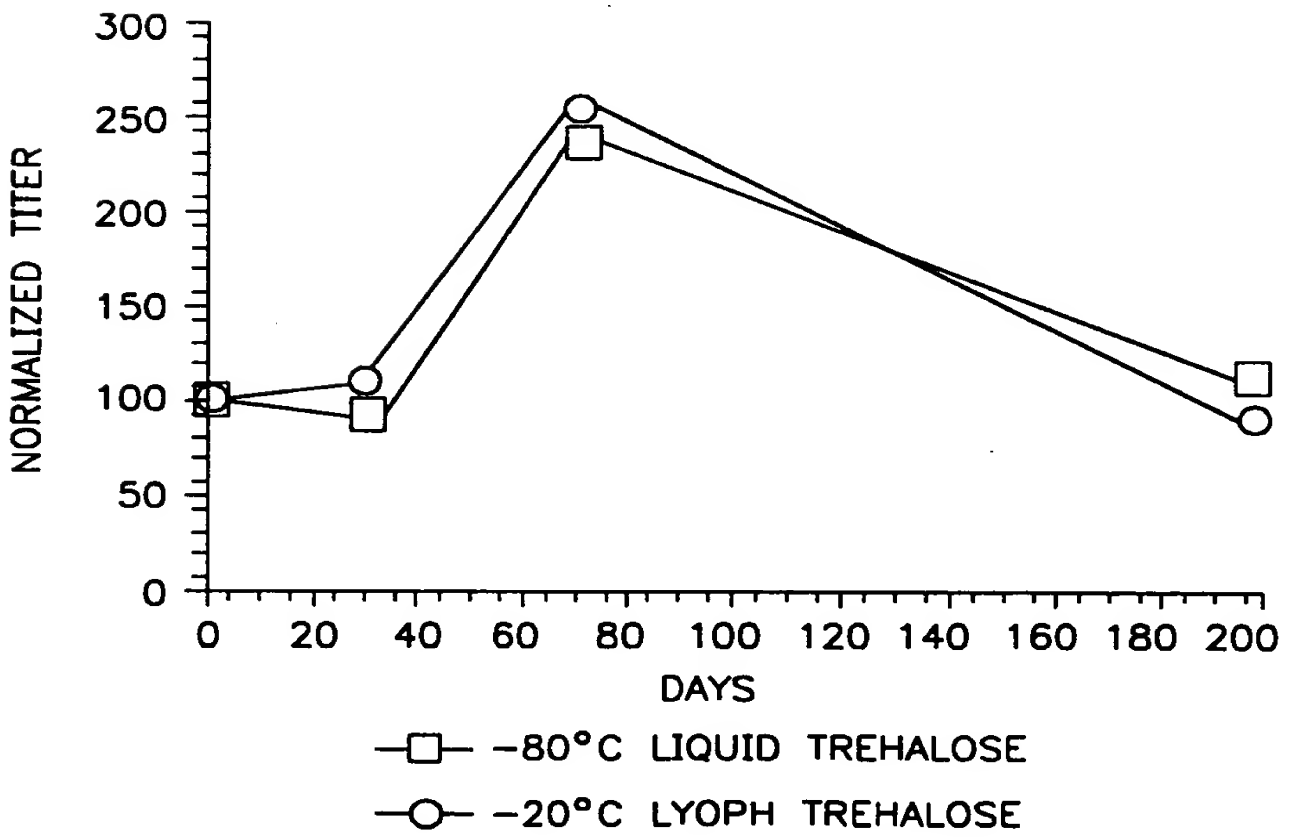


FIG. 16D

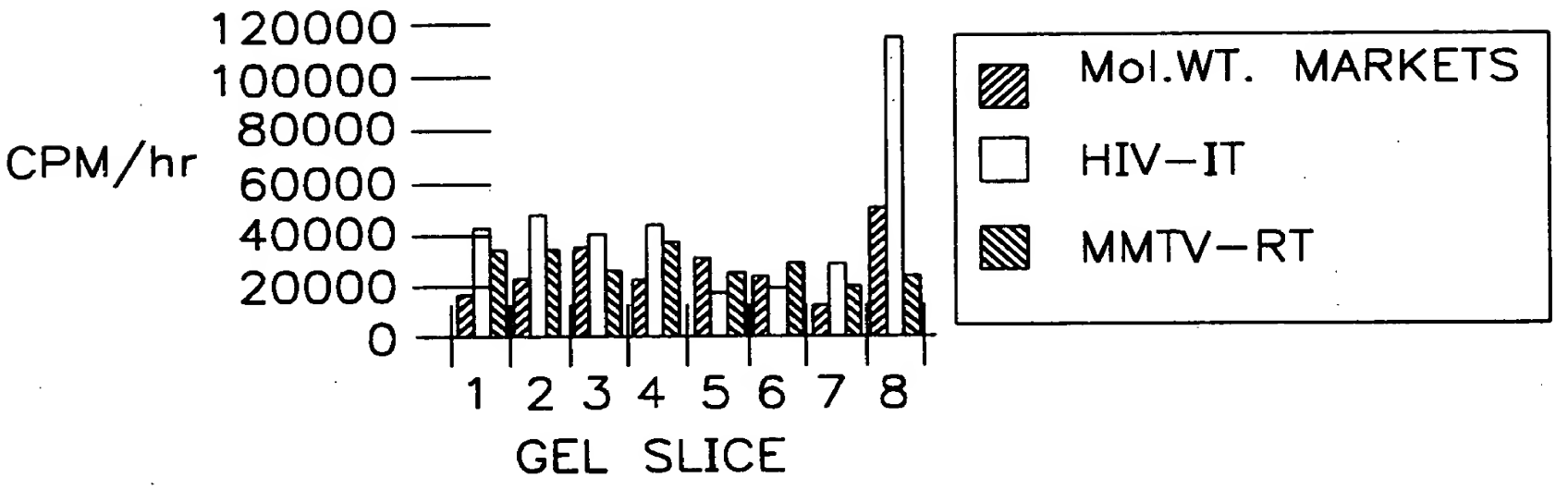


FIG. 17

FIG. 18

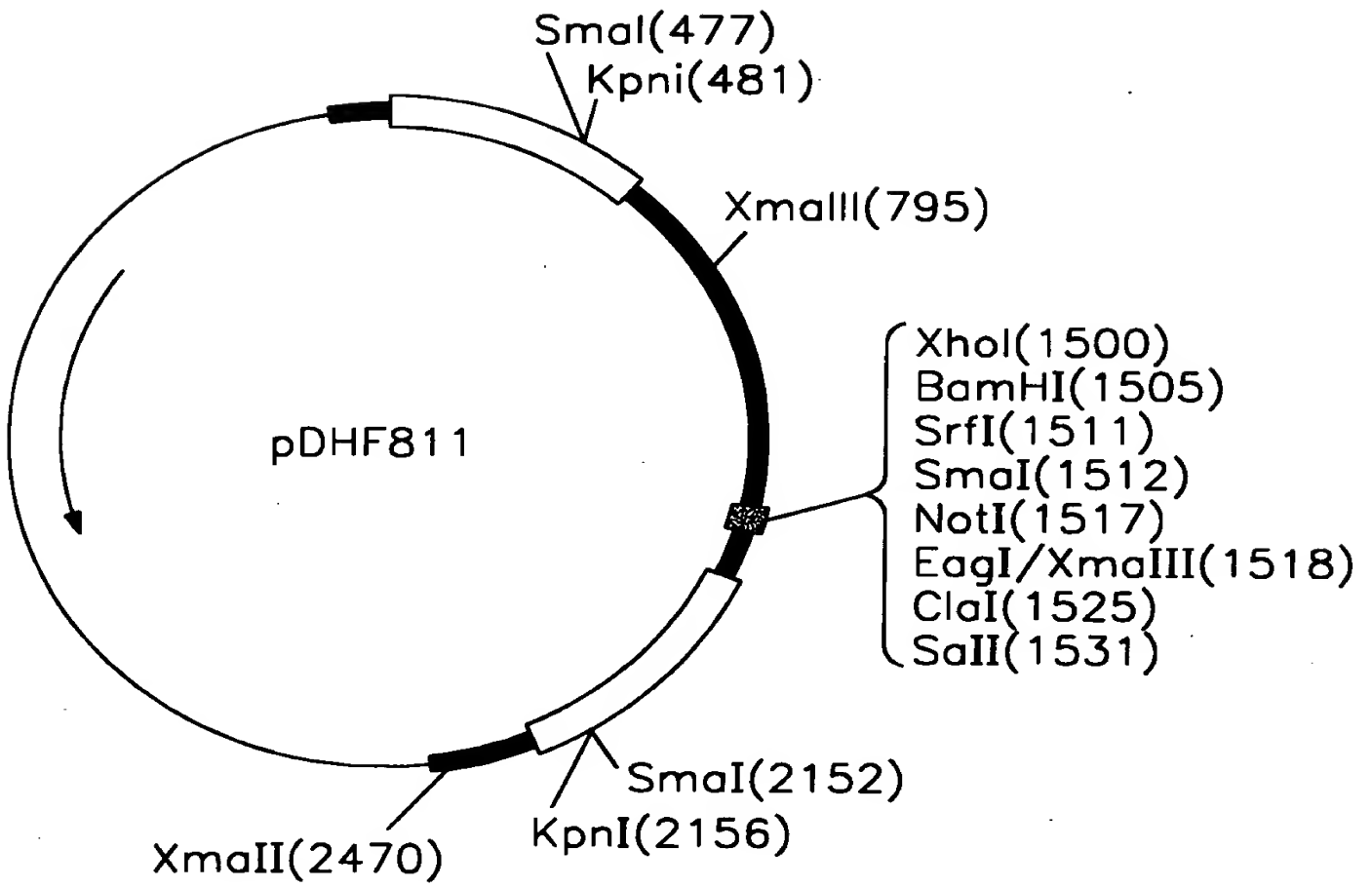


FIG. 19

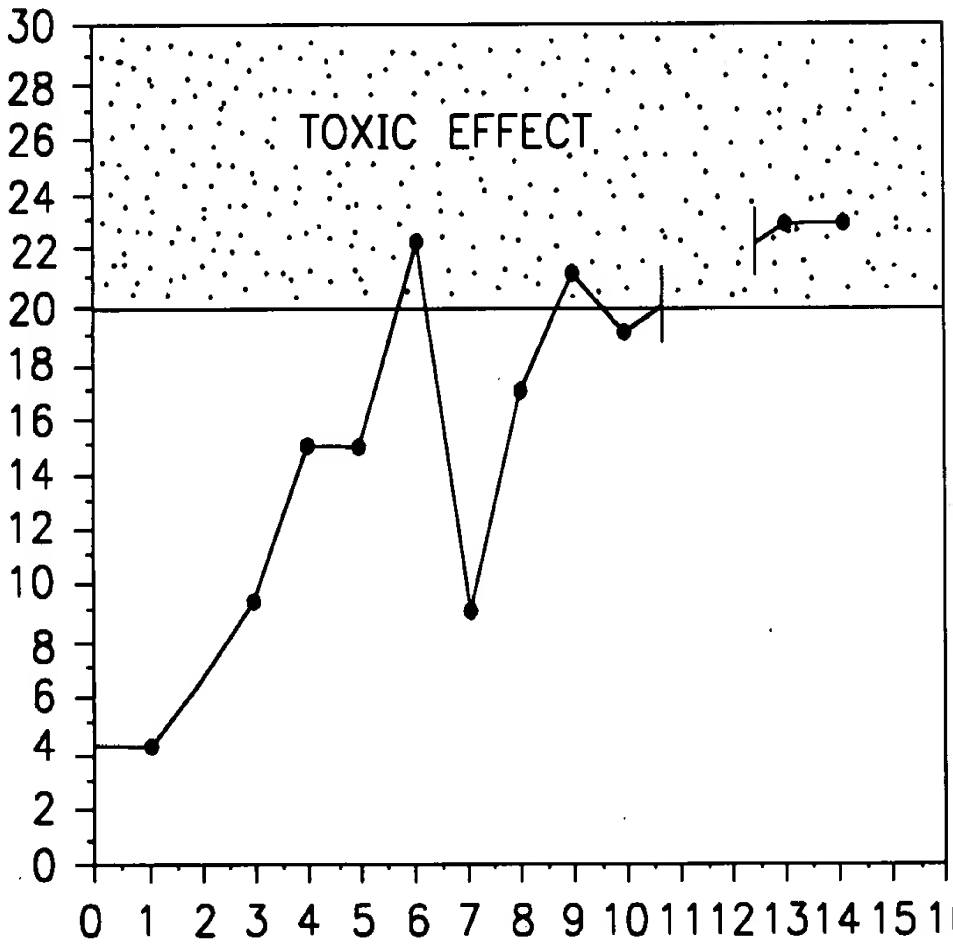


FIG. 20A

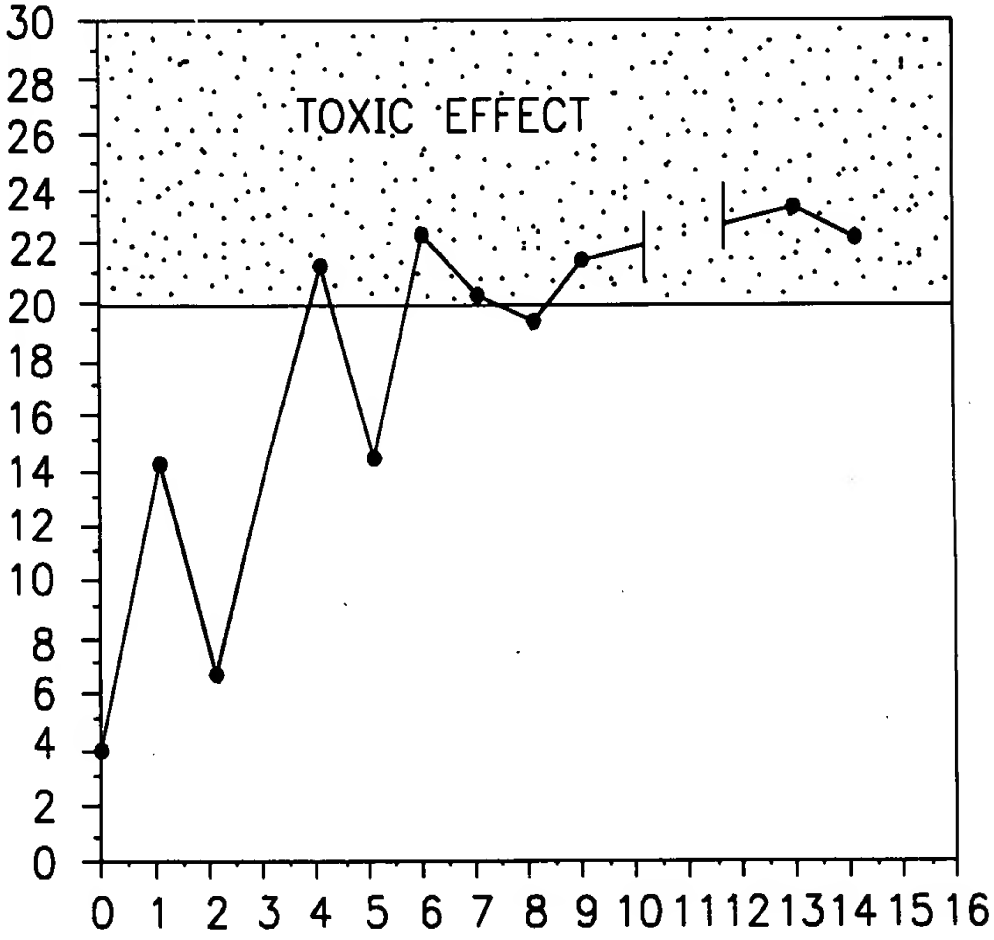


FIG. 20B

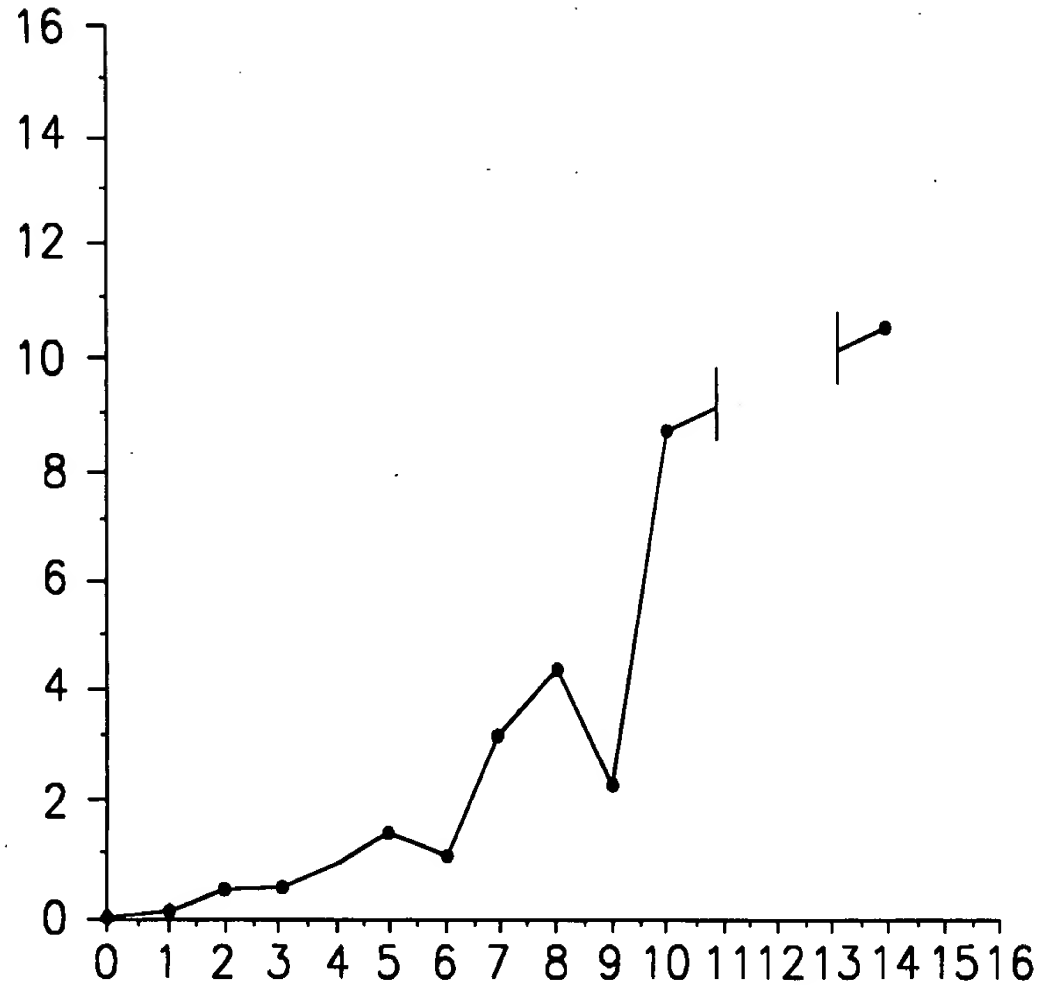


FIG. 20C

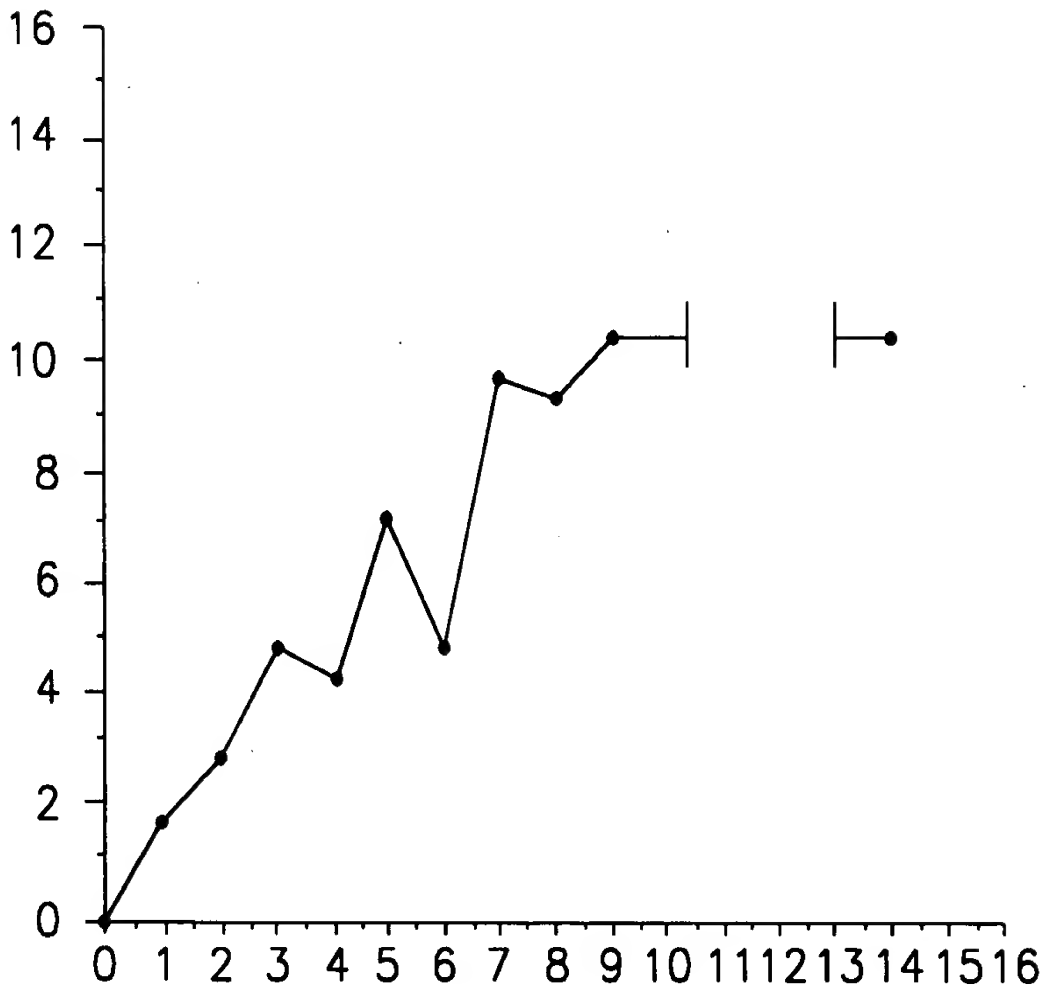


FIG. 20D

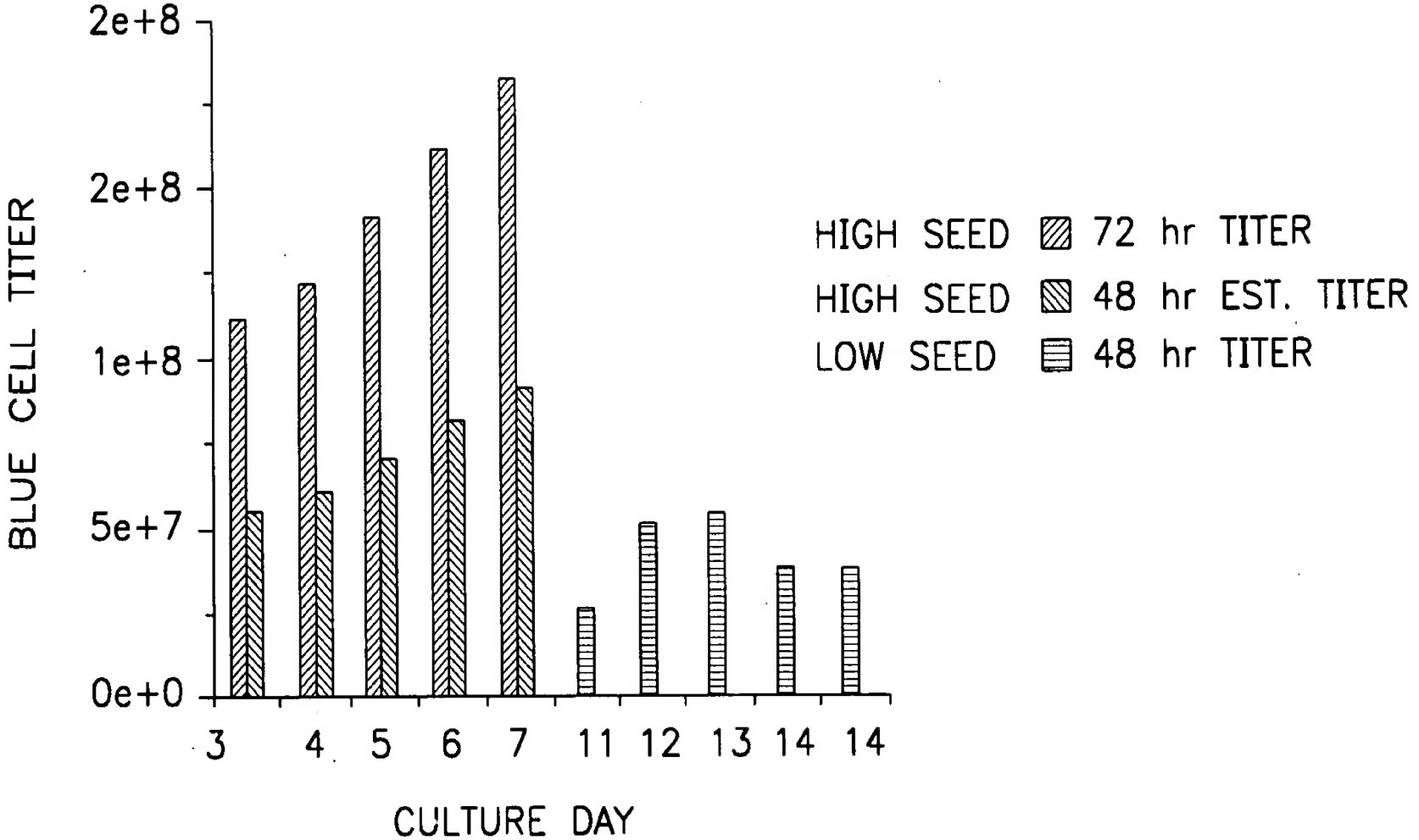


FIG. 21

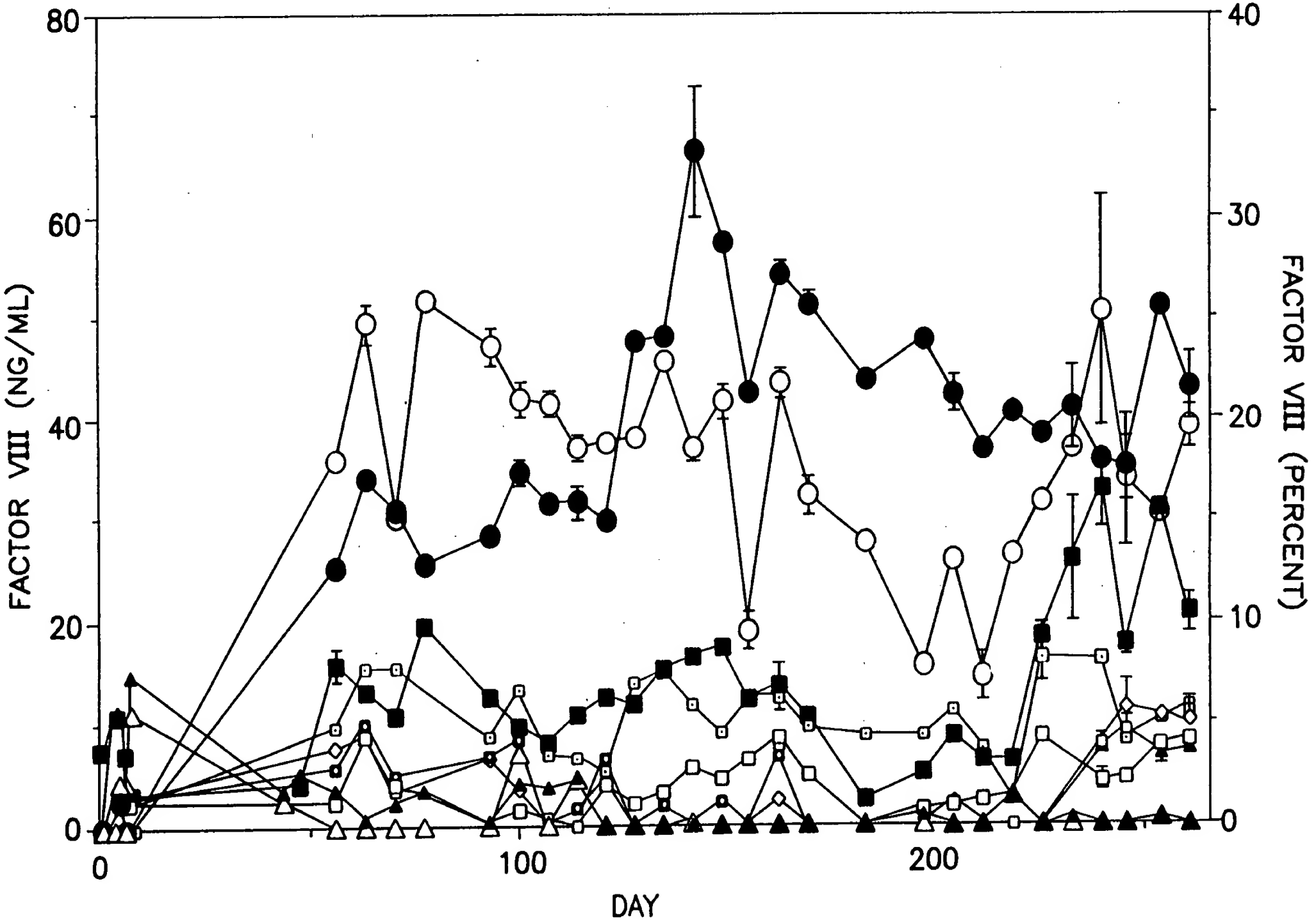


FIG. 22

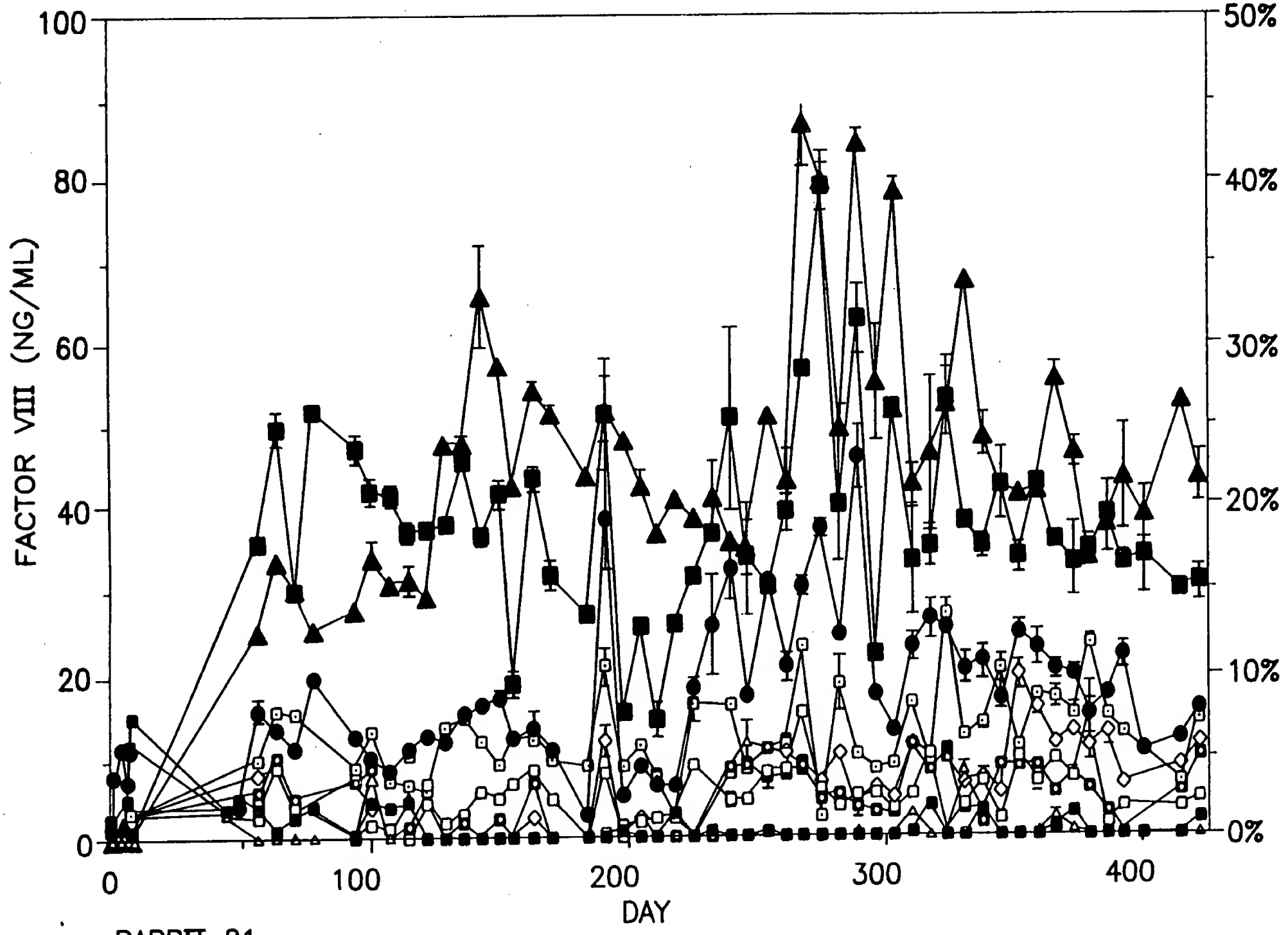


FIG. 23

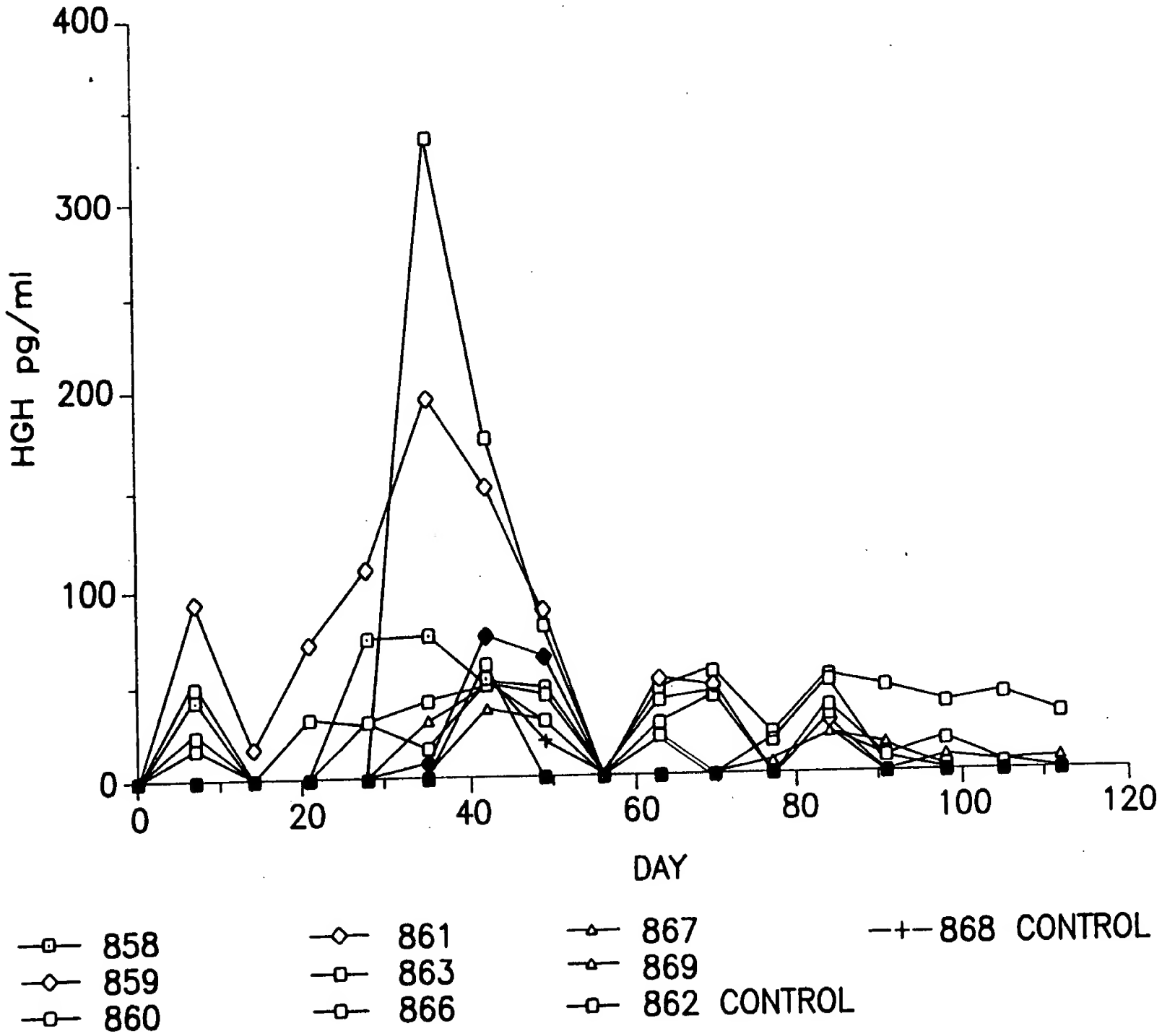


FIG. 24

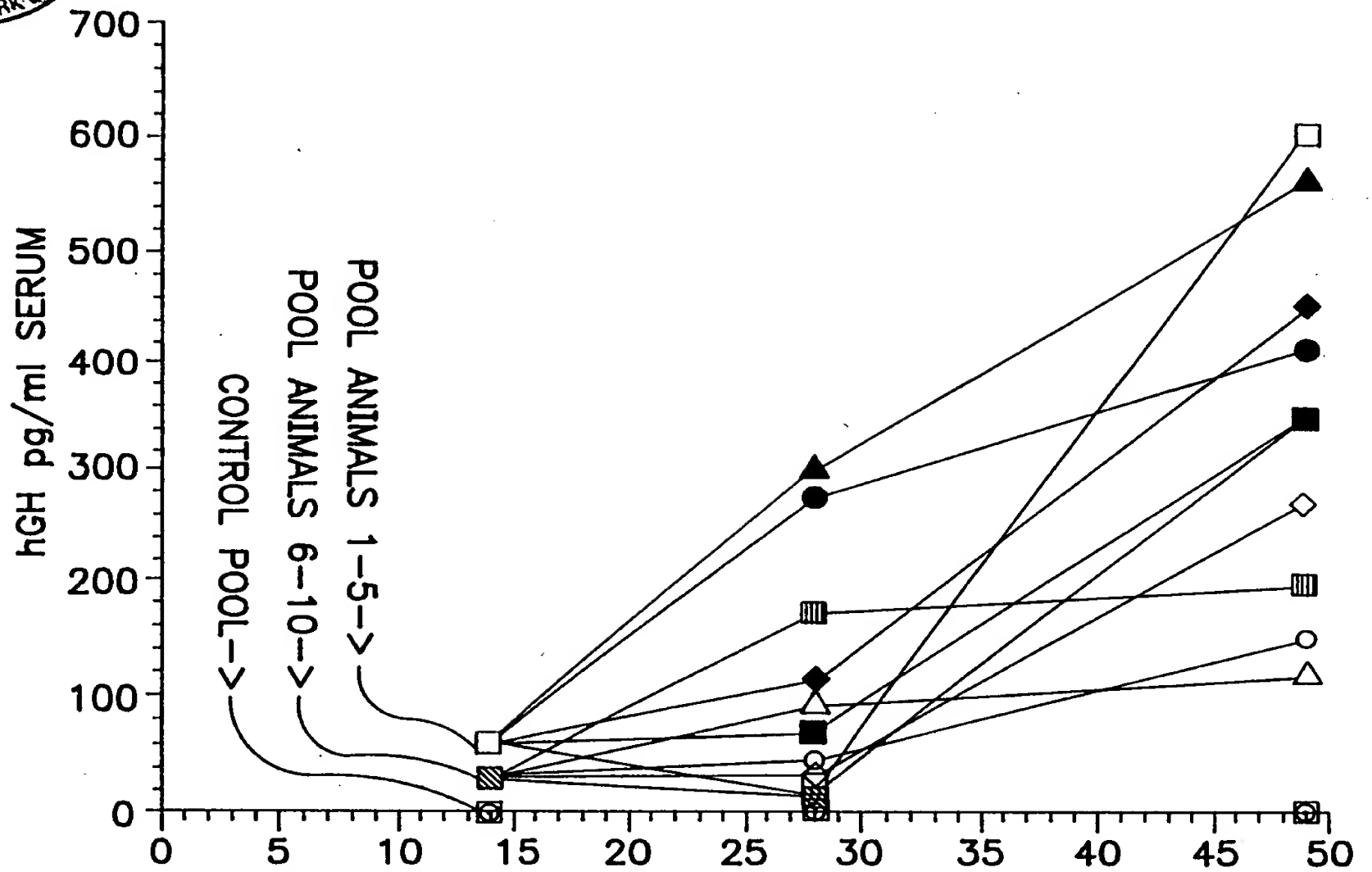


FIG. 25

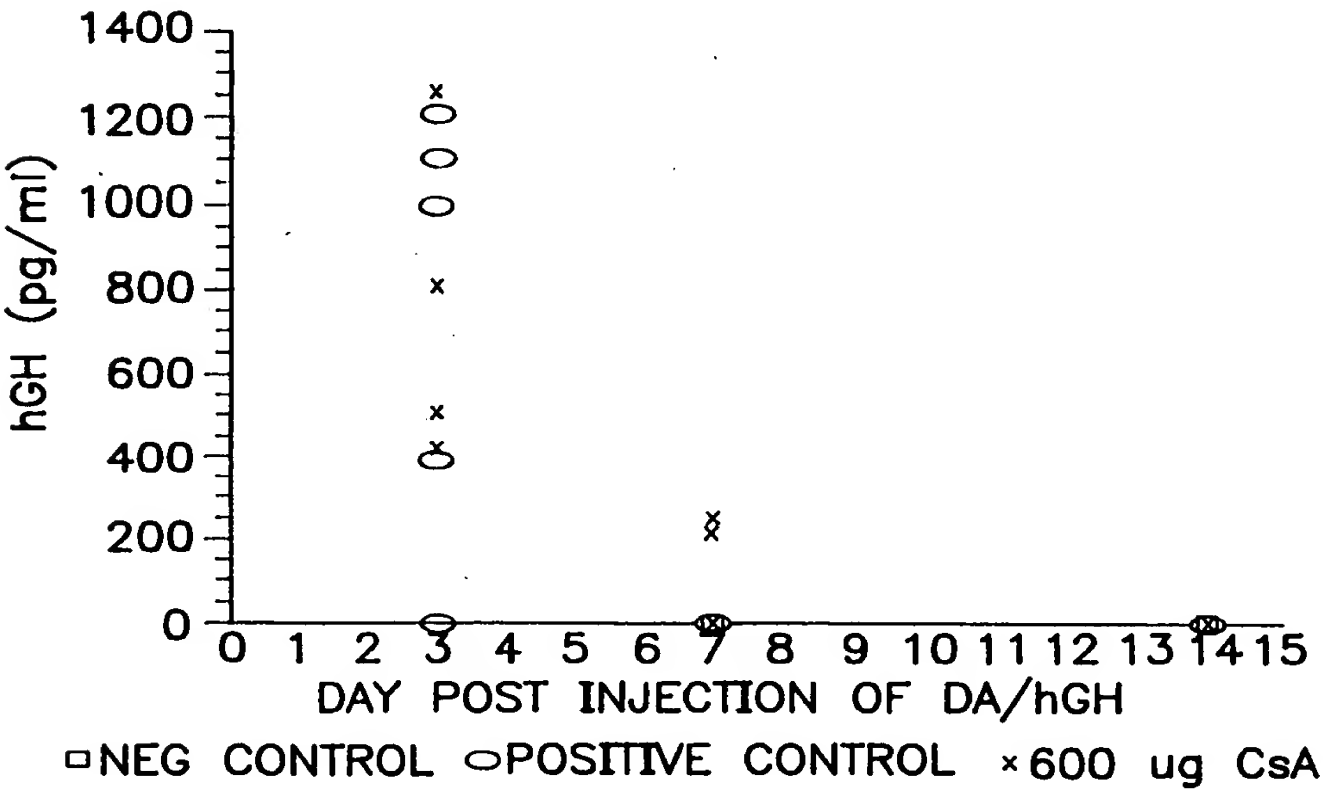


FIG. 26

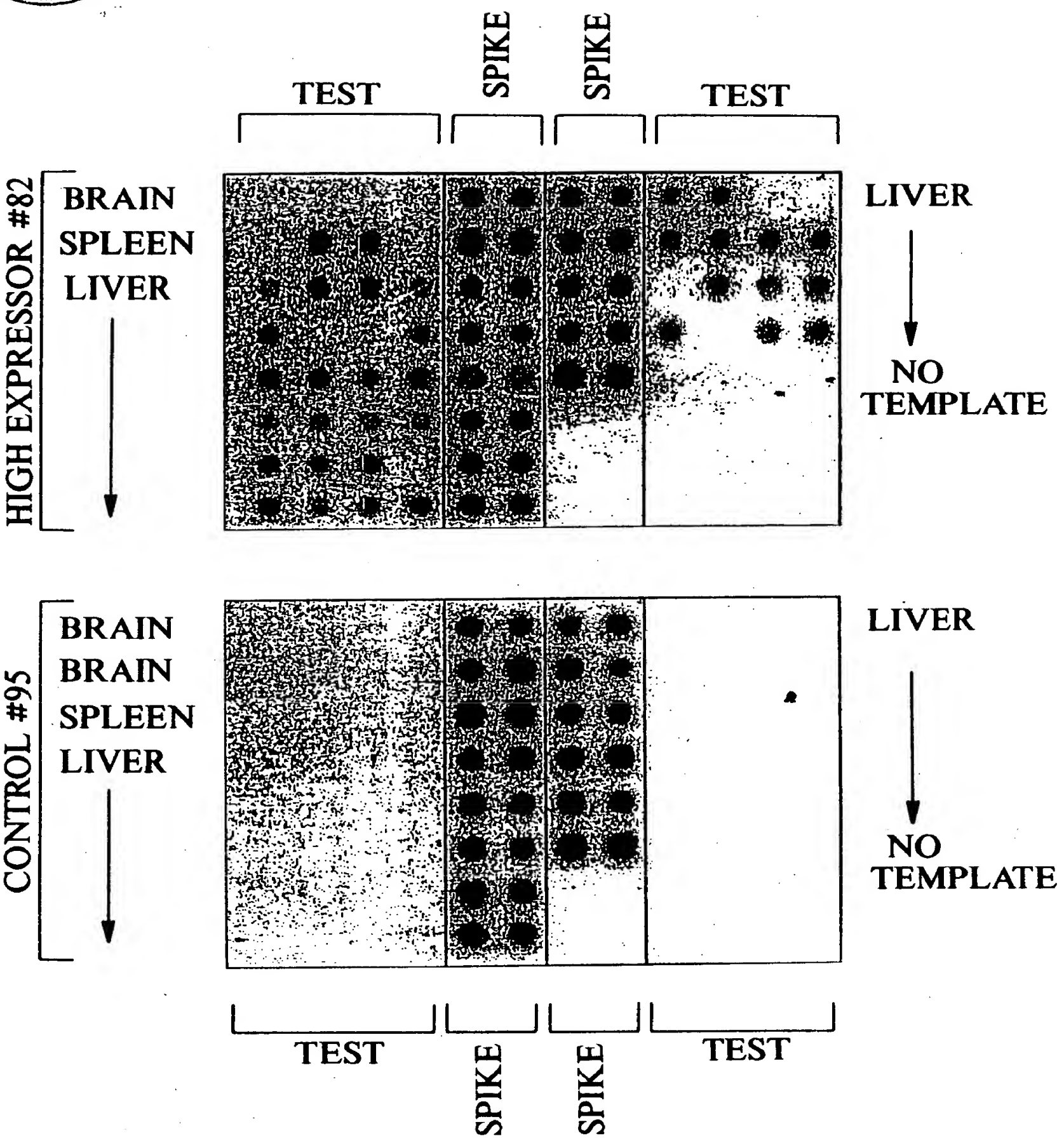


FIG 27

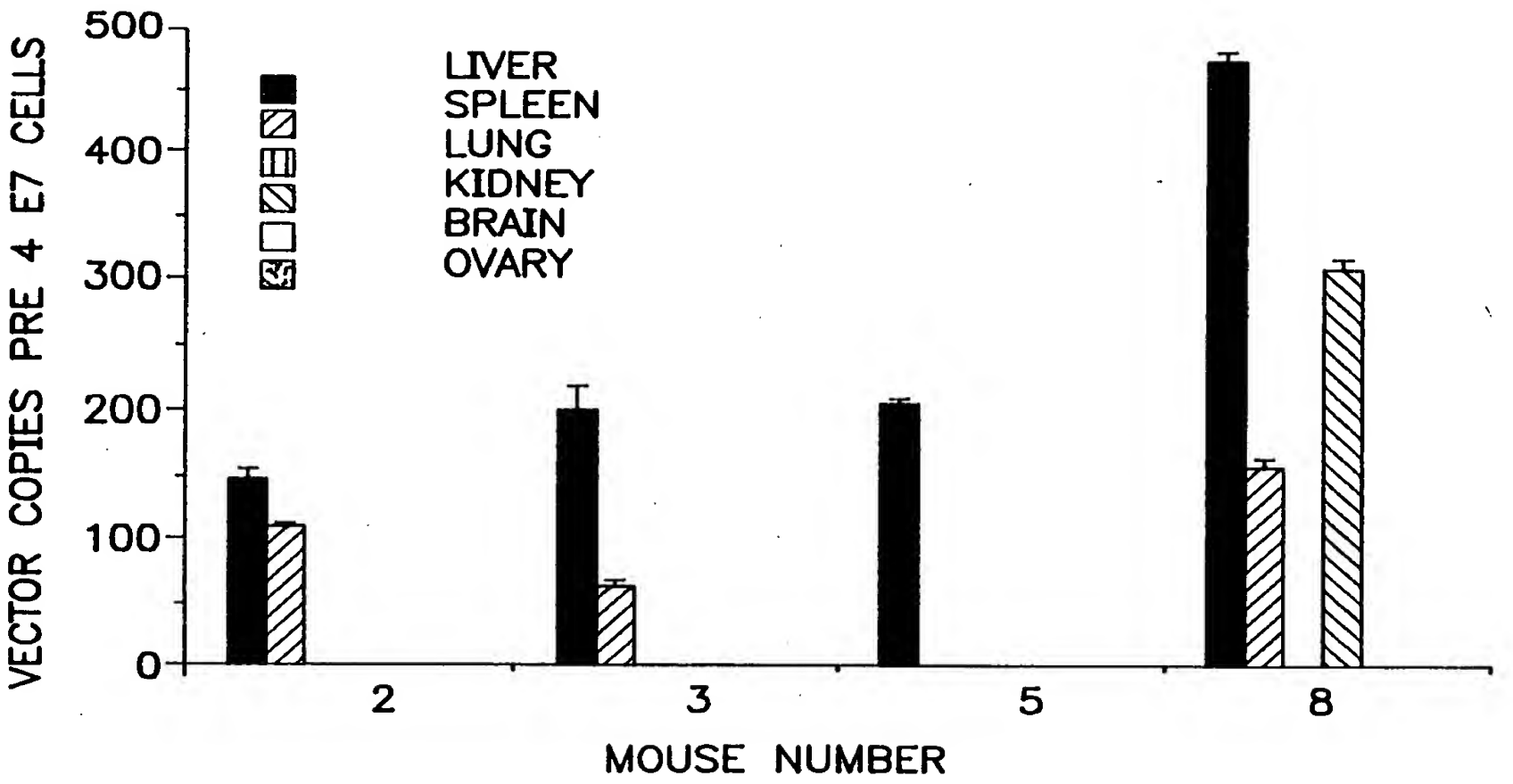


FIG. 28

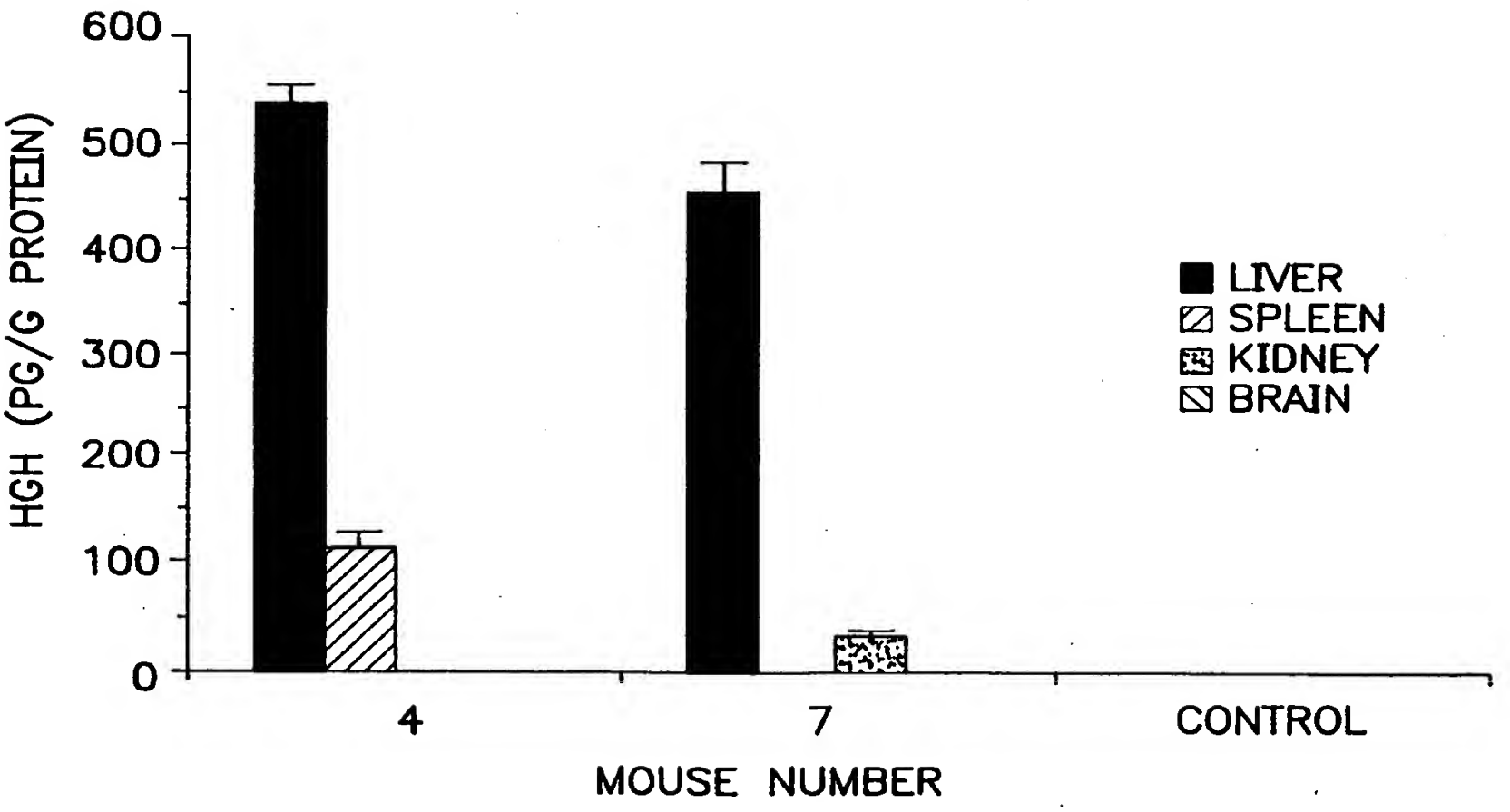


FIG. 29

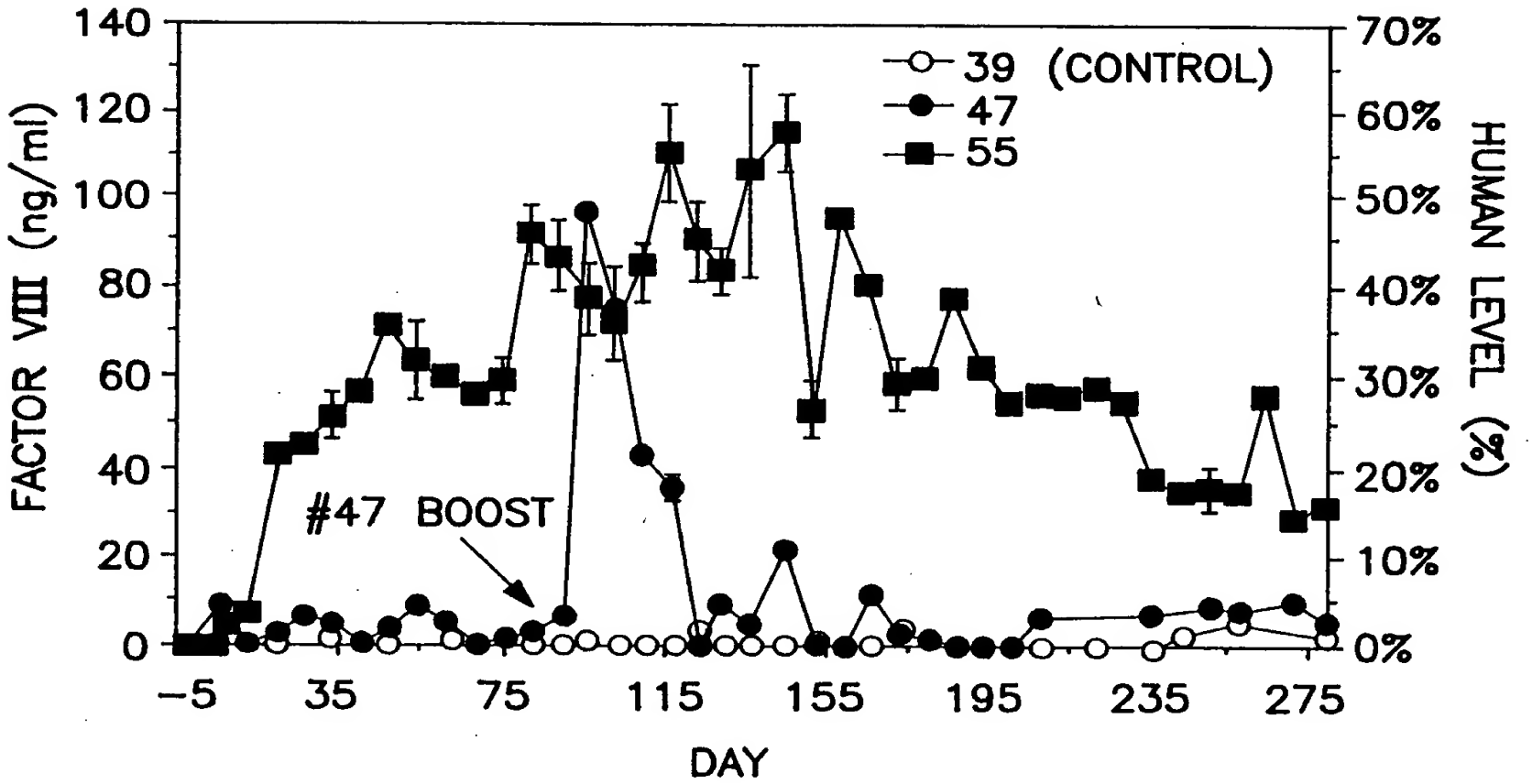


FIG. 30

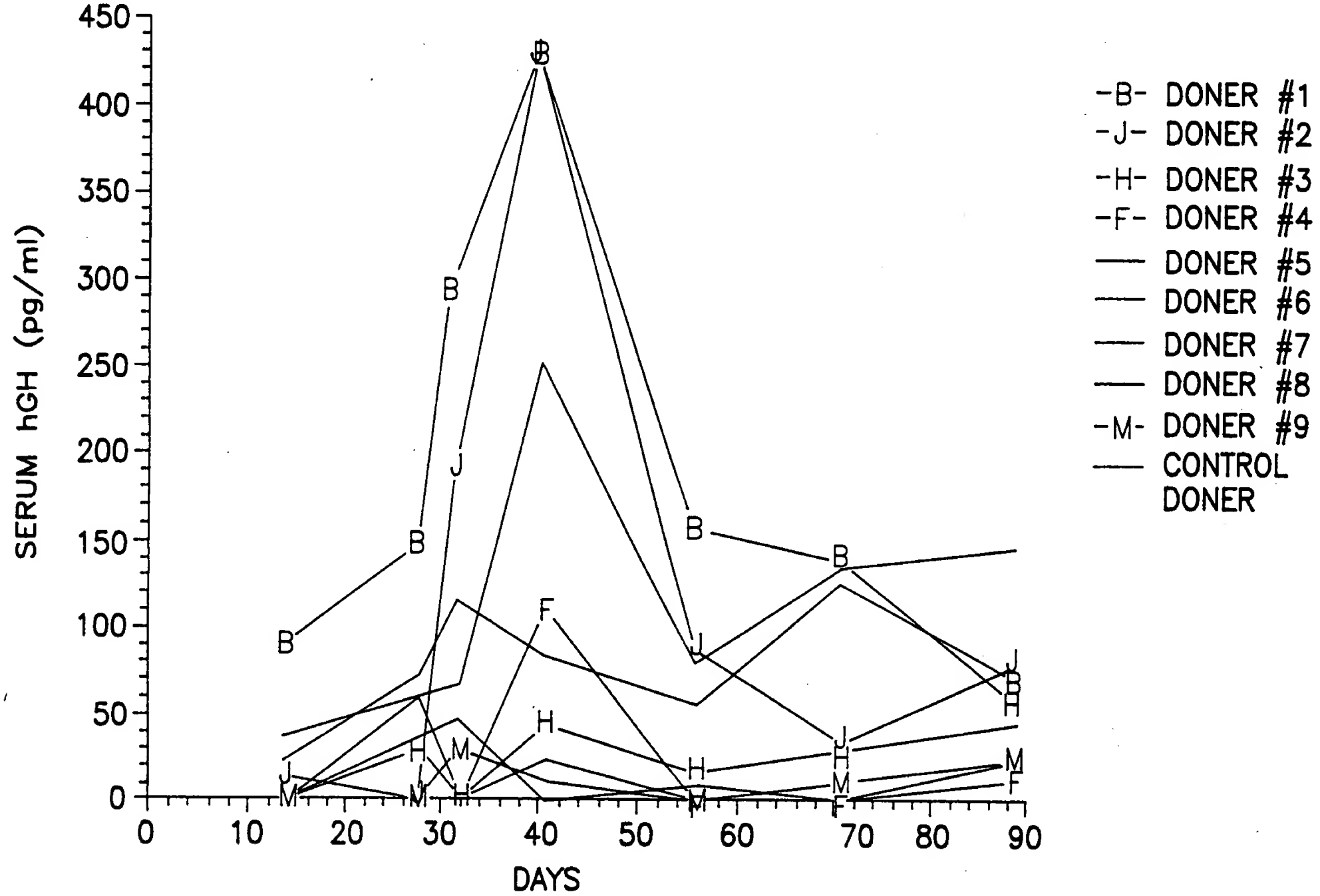


FIG. 31

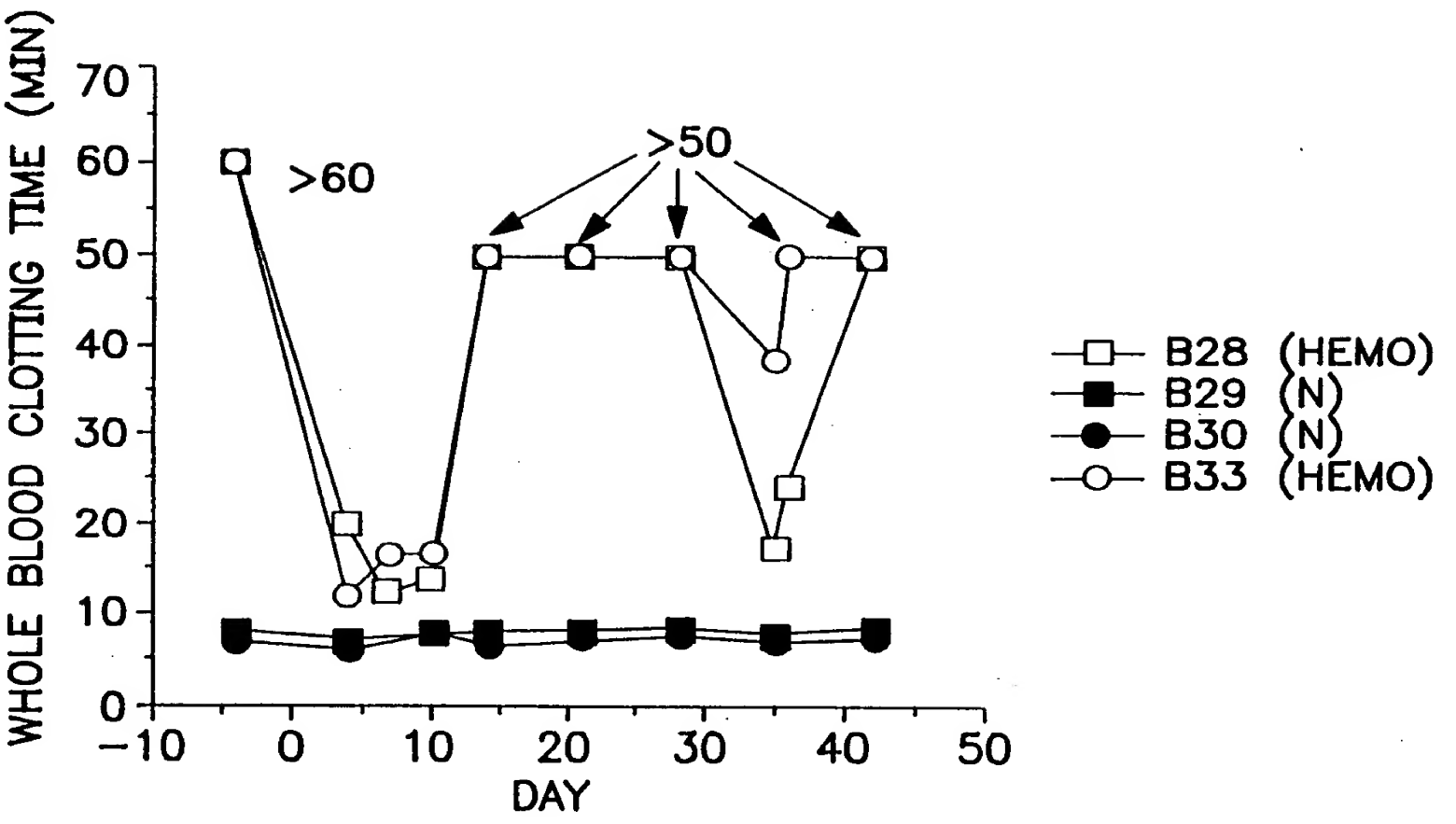


FIG. 32

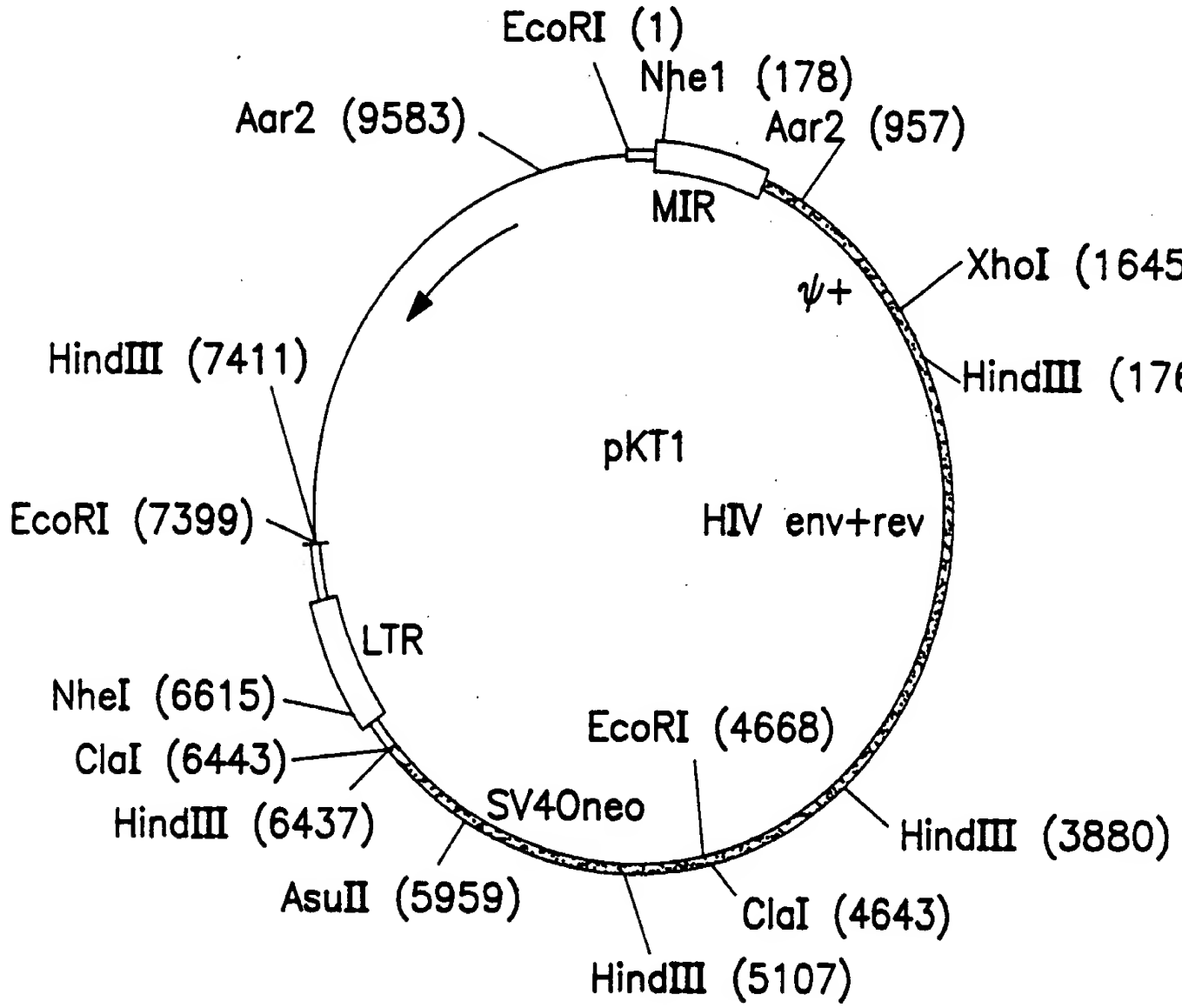
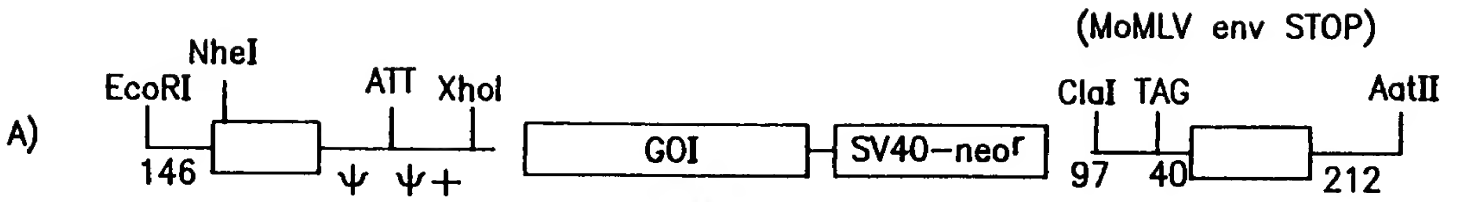


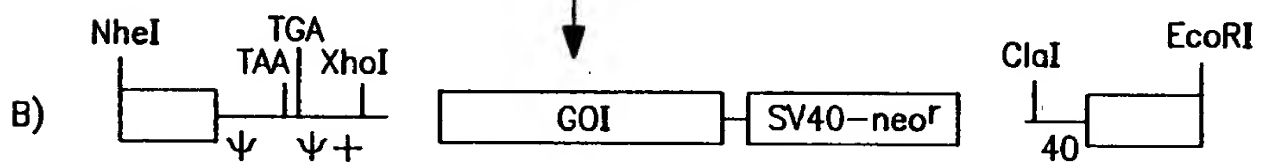
FIG. 33

RETROVIRAL BACKBONE (N2–DERIVED)



5' END: ATT TO TAA STOP, ADD SECOND STOP CONDON TGA, DELETE MoMLV SEQUENCES UPSTREAM OF 5'LTR (176 bp TOTAL)

3' END: DELETE 97 BASES OF MoMLV env SEQUENCE, DELETE 212 BASES OF MoMLV SEQUENCE DOWNSTREAM OF 3'LTR



CROSS–LESS RETROVIRAL BACKBONE: pBA–5

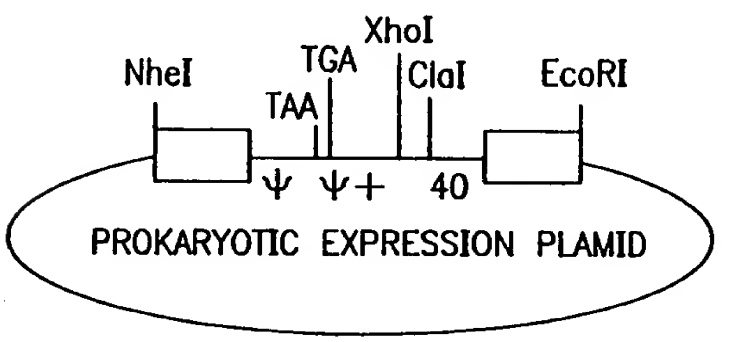


FIG. 34

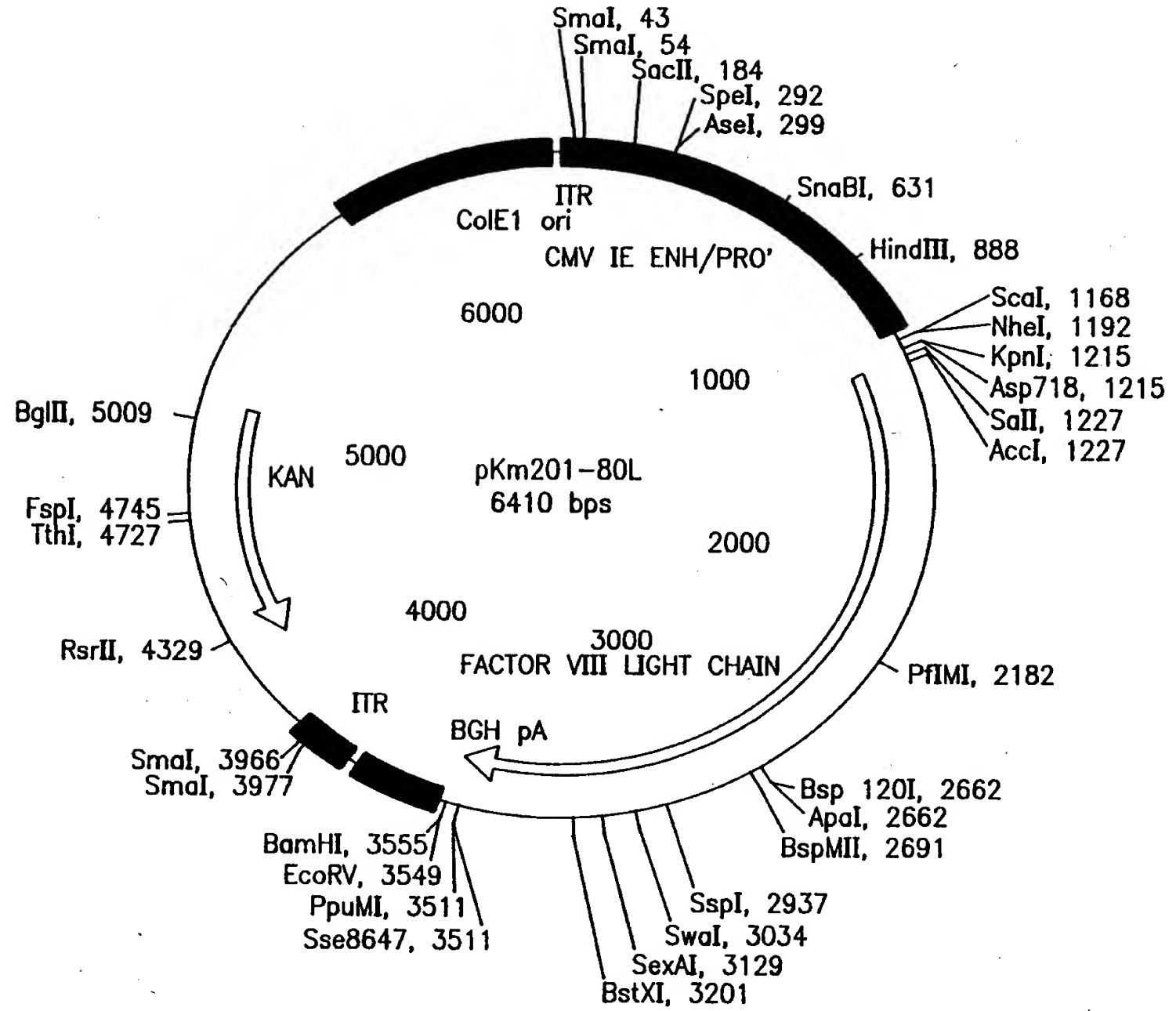


FIG. 35

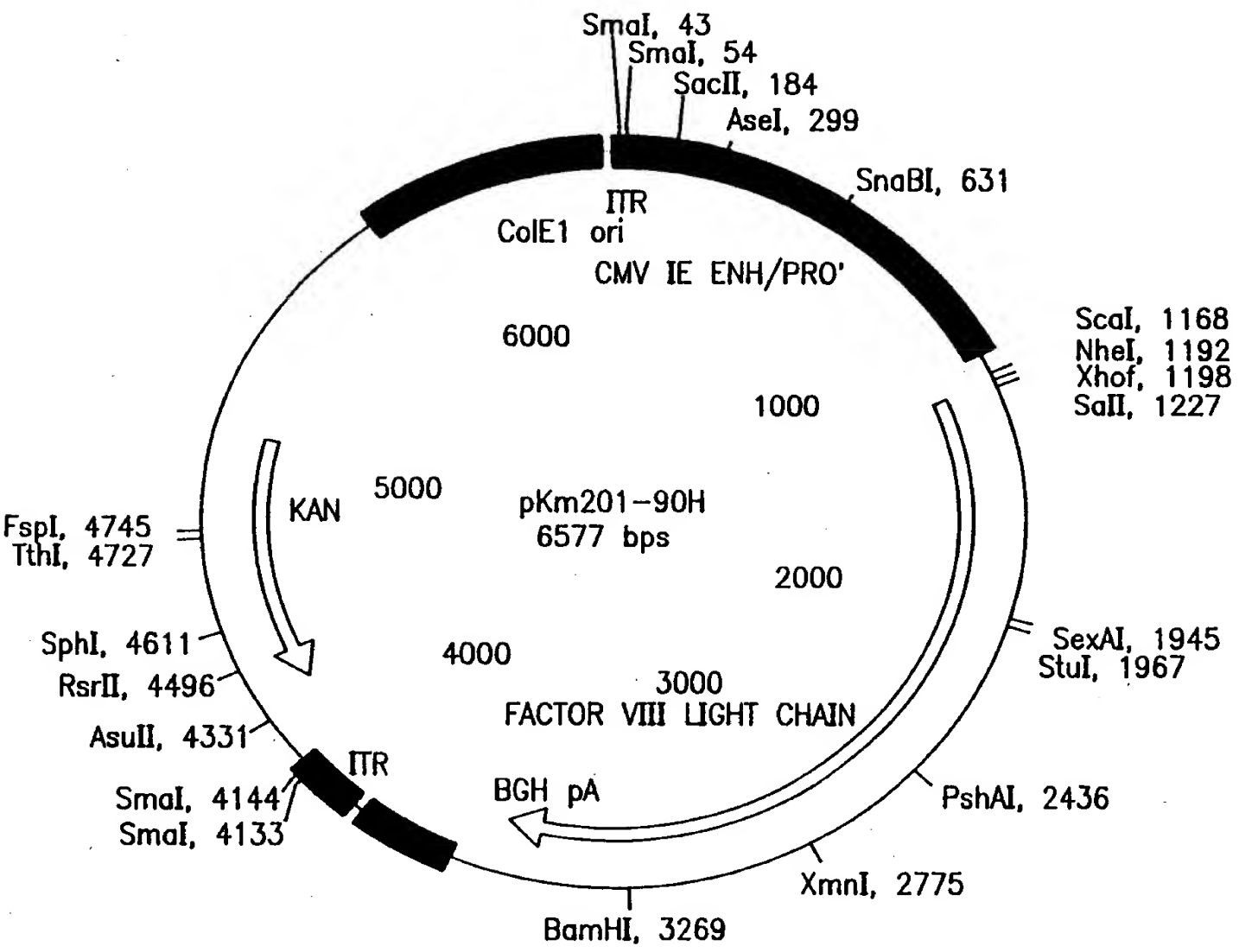


FIG. 36

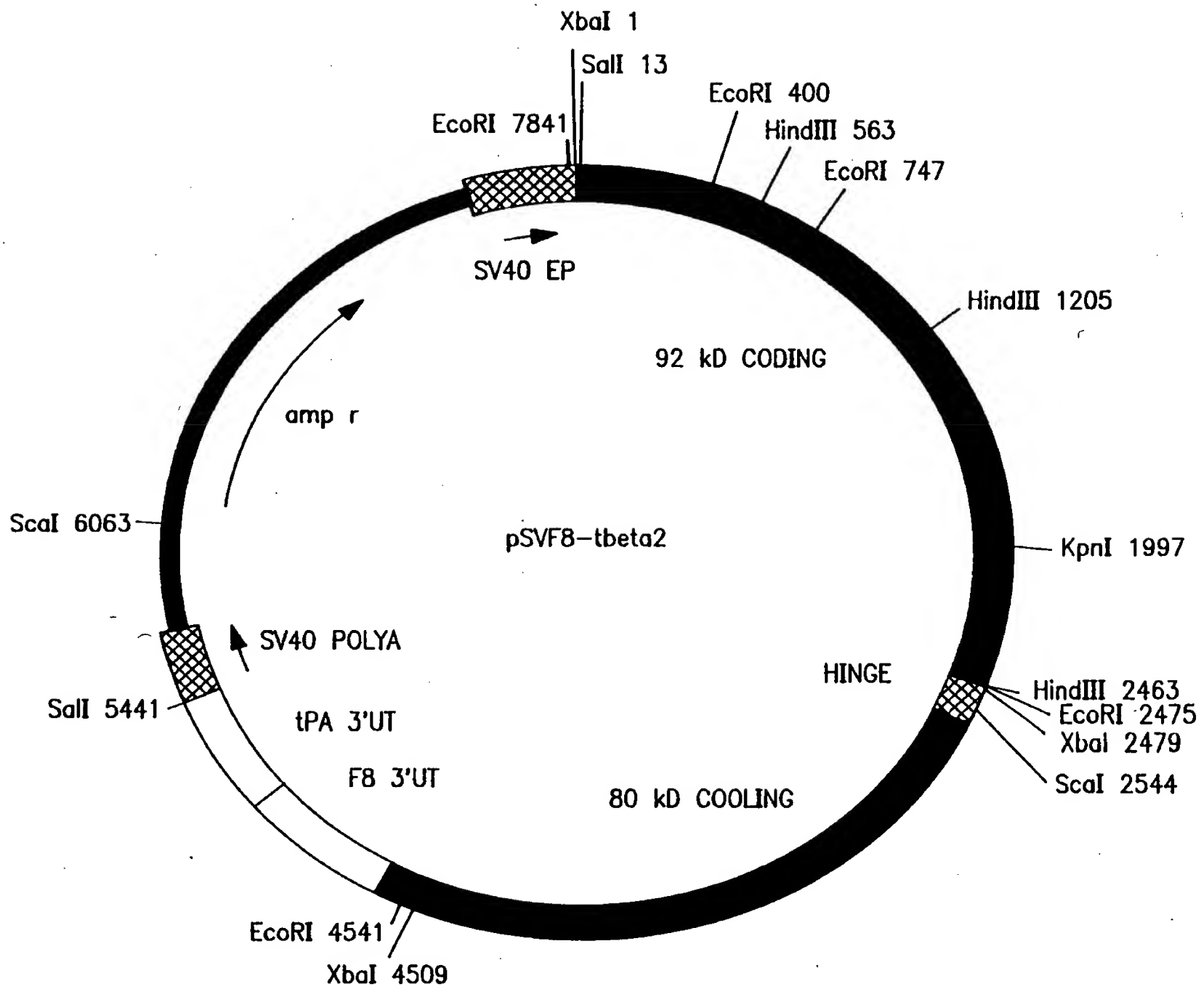


FIG. 37

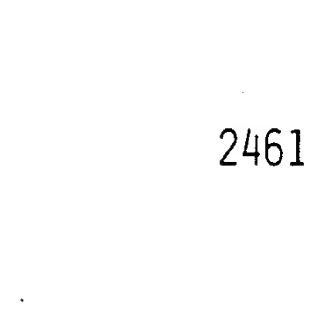
```
      ArgGlyMetThrAlaLeuLeuLysValSerSerCysAspLysAsnThrGlyAspTyrTyr  Seq ID No. 48
2341  AGAGGCATGACCGCCTTACTGAAGGTTTCTAGTTGTGACAAGAACACTGGTGATTATTAC  Seq ID No. 49
      TCTCCGTACTGGCGGAATGACTTCCAAAGATCAACACTGTTCTTGTGACCACTAATAATG

      GluAspSerTyrGluAspIleSerAlaTyrLeuLeuSerLysAsnAsnAlaIleGluPro
2401  GAGGACAGTTATGAAGATATTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCA
      CTCCTGTCAATACTTCTATAAAGTCGTATGAACGACTCATTTTTGTTACGGTAACTTGGT

         <----------N-terminus of beta domain------------------->

      ArgSerPheSerGlnAsnSerArgHisProSerThrArgGlnLysGlnPheAsnAlaThr
2461  AGAAGCTTCTCCCAGAATTCTAGACACCCTAGCACTAGGCAAAAGCAATTTAATGCCACC
      TCTTCGAAGAGGGTCTTAAGATCTGTGGGATCGTGATCCGTTTTCGTTAAATTACGGTGG
        ^                ^  ^
      2463 HIND3, 2475 ECORI, 2479 XBAI,

      <-- IgA hinge --->
```

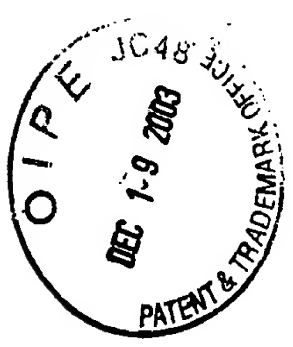


```
<-- C-term. beta domain -->

      ProProThrProProThrProProValLeuLysArgHisGlnArgGluIleThrArgThr
2521  CCTCCTACACCACCAACCCCACCAGTACTGAAACGCCATCAACGGGAAATAACTCGTACT
      GGAGGATGTGGTGGTTGGGGTGGTCATGACTTTGCGGTAGTTGCCCTTTATTGAGCATGA
                              ^
                    2544 SCAI,

      ThrLeuGlnSerAspGlnGluGluIleAspTyrAspAspThrIleSerValGluMetLys
2581  ACTCTTCAGTCTGATCAAGAGGAAATTGACTATGATGATACCATATCAGTTGAAATGAAG
      TGAGAAGTCAGACTAGTTCTCCTTTAACTGATACTACTATGGTATAGTCAACTTTACTTC
                 ^
          2592 BCLI,
```

FIG. 38



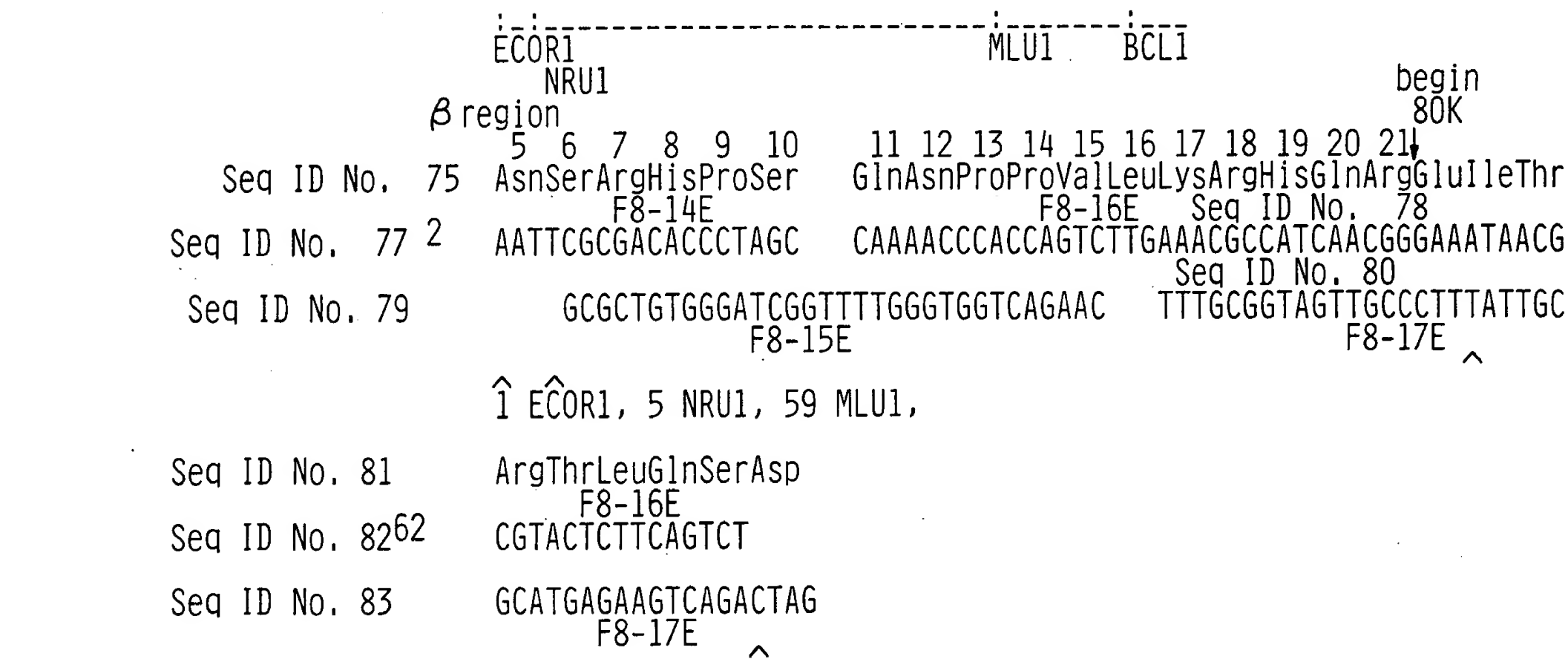


FIG. 39

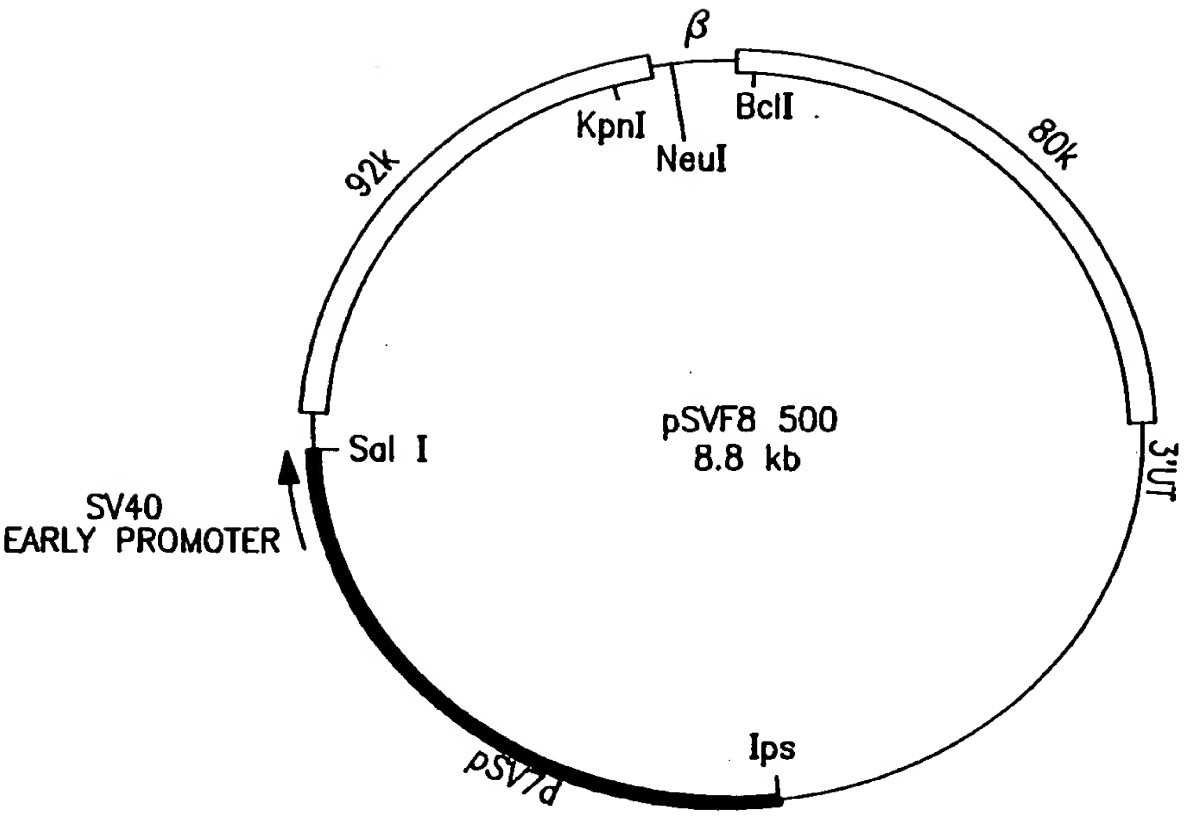


FIG. 40A

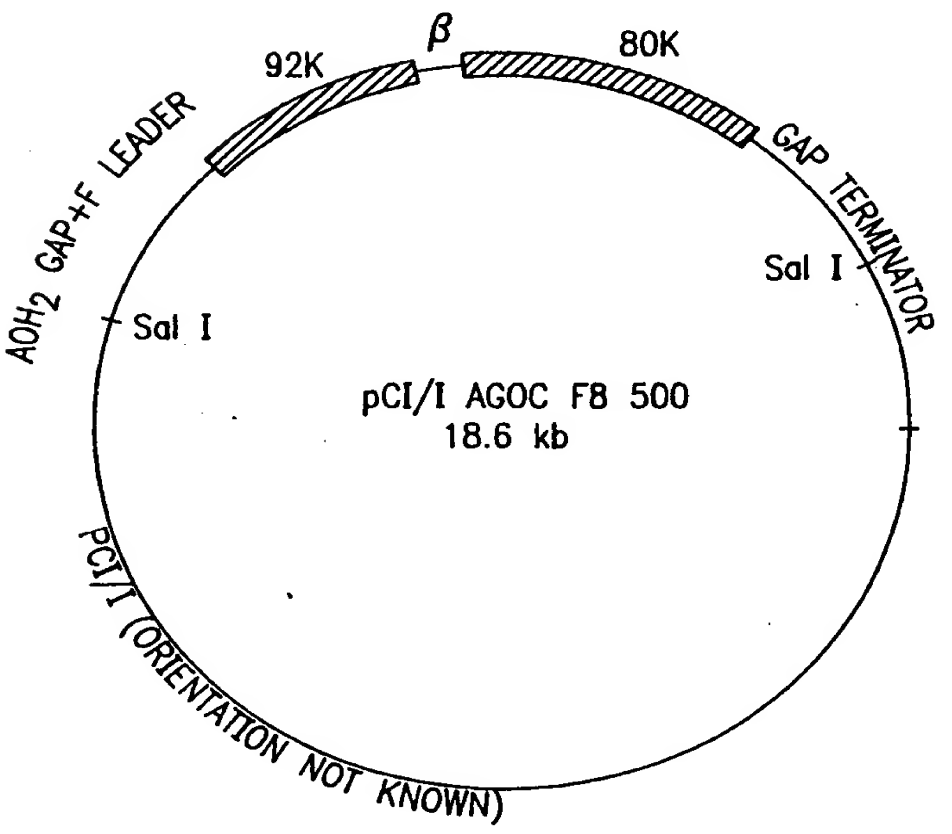


FIG. 40B

Linkers for pSVF8-500B

end 92 19aa C terminal
to thrombin cleavage at 740

SerArgHisProSerThrArgGlnLysGlnPheAsnAlaThrProProValLeuLysArg Seq ID No. 50
TCGCGACACCCTAGCACTAGGCAAAAGCAATTTAATGCCACCCCACCAGTCCTGAAACGC Seq ID No. 51
mutant AGCGCTGTGGGATCGTGATCCGTTTTCGTTAAATTACGGTGGGGTGGTCATGACTTTGCG
wild type (TT) (CT)
NRU1

Start 80K
HisGlnArgGluIleThrArg
CATCAACGGGAAATAACGCGT
GTAGTTGCCCTTTATTGCGCA

MLU1
9aa N terminal to 80K

FIG. 41